

(FILE 'HOME' ENTERED AT 21:08:12 ON 02 AUG 2006)

FILE 'MEDLINE, BIOSIS, CAPLUS, EMBASE, SCISEARCH' ENTERED AT 21:08:27 ON
02 AUG 2006

L1 16489 SEA ABB=ON PLU=ON MCCREADY P?/AU OR RADNEDGE L?/AU OR
ANDERSON G?/AU OR OTT L?/AU OR SLEZAK T?/AU OR KUCZMARSKI
T?/AU OR MOTIN V?/AU

L2 172 SEA ABB=ON PLU=ON L1 AND PESTIS

L3 37 SEA ABB=ON PLU=ON L2 AND (PRIMER OR PROBE OR PCR)

L4 16 DUP REM L3 (21 DUPLICATES REMOVED)
D L4 BIB ABS 1-16

L5 256 SEA ABB=ON PLU=ON PESTIS (50W) (PROBE OR PRIMER OR PCR)

L6 150 SEA ABB=ON PLU=ON L5 AND DETECT?

L7 82 DUP REM L6 (68 DUPLICATES REMOVED)

EAST Search History

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	257	mcready-p\$.in. radnedge-l\$.in. andersen-g\$.in. ott-l\$.in. slezak-t\$.in. kuczmarski-t\$.in. motin-v\$.in.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/08/02 21:13
L2	11	l and pestis	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/08/02 21:13
L3	131	Pestis same (primer probe PCR)	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/08/02 21:14
L4	57	3 same (detect\$8 determin\$8 identif\$8)	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/08/02 21:14

AF053947/c

LOCUS AF053947 100984 bp DNA circular BCT 17-JUN-2003

DEFINITION Yersinia pestis KIM plasmid pMT1, complete sequence.

ACCESSION AF053947

VERSION AF053947.1 GI:2996286

KEYWORDS .

SOURCE Yersinia pestis KIM

ORGANISM Yersinia pestis KIM

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Yersinia.

REFERENCE 1 (bases 1 to 100984)

AUTHORS Hu, P., Elliott, J., McCready, P., Skowronski, E., Garnes, J., Kobayashi, A., Brubaker, R.R. and Garcia, E.

TITLE Structural organization of virulence-associated plasmids of Yersinia pestis

JOURNAL J. Bacteriol. 180 (19), 5192-5202 (1998)

PUBMED 9748454

REFERENCE 2 (bases 1 to 100984)

AUTHORS Hu, P., Elliott, J., McCready, P., Skowronski, E., Garnes, J., Kobayashi, A., Carrano, A.V., Brubaker, R. and Garcia, E.

TITLE Direct Submission

JOURNAL Submitted (16-MAR-1998) Biology and Biotechnology Research, Lawrence Livermore National Lab, L452, 7000 East Ave., Livermore, CA 94550, USA

FEATURES Location/Qualifiers

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Query Match 100.0%; Score 28; DB 15; Length 100984;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 5
 AF053947

LOCUS AF053947 100984 bp DNA circular BCT 17-JUN-2003

DEFINITION Yersinia pestis KIM plasmid pMT1, complete sequence.

ACCESSION AF053947

VERSION AF053947.1 GI:2996286

KEYWORDS .

SOURCE Yersinia pestis KIM

ORGANISM Yersinia pestis KIM

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Yersinia.

REFERENCE 1 (bases 1 to 100984)

AUTHORS Hu, P., Elliott, J., McCready, P., Skowronski, E., Garnes, J., Kobayashi, A., Brubaker, R.R. and Garcia, E.

TITLE Structural organization of virulence-associated plasmids of Yersinia pestis

JOURNAL J. Bacteriol. 180 (19), 5192-5202 (1998)

PUBMED 9748454

REFERENCE 2 (bases 1 to 100984)

AUTHORS Hu, P., Elliott, J., McCready, P., Skowronski, E., Garnes, J., Kobayashi, A., Carrano, A.V., Brubaker, R. and Garcia, E.

TITLE Direct Submission

JOURNAL Submitted (16-MAR-1998) Biology and Biotechnology Research, Lawrence Livermore National Lab, L452, 7000 East Ave., Livermore, CA 94550, USA

FEATURES Location/Qualifiers

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Query Match 100.0%; Score 28; DB 15; Length 100984;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 5
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LOCUS AF053947 100984 bp DNA circular BCT 17-JUN-2003

DEFINITION Yersinia pestis KIM plasmid pMT1, complete sequence.

ACCESSION AF053947

VERSION AF053947.1 GI:2996286

KEYWORDS .

SOURCE Yersinia pestis KIM

ORGANISM Yersinia pestis KIM

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Yersinia.

REFERENCE 1 (bases 1 to 100984)

AUTHORS Hu, P., Elliott, J., McCready, P., Skowronski, E., Garnes, J., Kobayashi, A., Brubaker, R.R. and Garcia, E.

TITLE Structural organization of virulence-associated plasmids of Yersinia pestis

JOURNAL J. Bacteriol. 180 (19), 5192-5202 (1998)

PUBMED 9748454

REFERENCE 2 (bases 1 to 100984)

AUTHORS Hu, P., Elliott, J., McCready, P., Skowronski, E., Garnes, J., Kobayashi, A., Carrano, A.V., Brubaker, R. and Garcia, E.

TITLE Direct Submission

JOURNAL Submitted (16-MAR-1998) Biology and Biotechnology Research, Lawrence Livermore National Lab, L452, 7000 East Ave., Livermore, CA 94550, USA

FEATURES Location/Qualifiers

source 1. .100984

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Best Local Similarity 100.0%; Pred. No. 5.6e-05;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4
 AF053947/c

LOCUS AF053947 100984 bp DNA circular BCT 17-JUN-2003

DEFINITION Yersinia pestis KIM plasmid pMT1, complete sequence.

ACCESSION AF053947

VERSION AF053947.1 GI:2996286

KEYWORDS .

SOURCE Yersinia pestis KIM

ORGANISM Yersinia pestis KIM

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Yersinia.

REFERENCE 1 (bases 1 to 100984)

AUTHORS Hu, P., Elliott, J., McCready, P., Skowronski, E., Garnes, J., Kobayashi, A., Brubaker, R.R. and Garcia, E.

TITLE Structural organization of virulence-associated plasmids of Yersinia pestis

JOURNAL J. Bacteriol. 180 (19), 5192-5202 (1998)

PUBMED 9748454

REFERENCE 2 (bases 1 to 100984)

AUTHORS Hu, P., Elliott, J., McCready, P., Skowronski, E., Garnes, J., Kobayashi, A., Carrano, A.V., Brubaker, R. and Garcia, E.

TITLE Direct Submission

JOURNAL Submitted (16-MAR-1998) Biology and Biotechnology Research, Lawrence Livermore National Lab, L452, 7000 East Ave., Livermore, CA 94550, USA

FEATURES Location/Qualifiers

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RESULT 4
 AF053947

LOCUS AF053947 100984 bp DNA circular BCT 17-JUN-2003

DEFINITION Yersinia pestis KIM plasmid pMT1, complete sequence.

ACCESSION AF053947

VERSION AF053947.1 GI:2996286

KEYWORDS .

SOURCE Yersinia pestis KIM

ORGANISM Yersinia pestis KIM

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Yersinia.

REFERENCE 1 (bases 1 to 100984)

AUTHORS Hu, P., Elliott, J., McCready, P., Skowronski, E., Garnes, J., Kobayashi, A., Brubaker, R.R. and Garcia, E.

TITLE Structural organization of virulence-associated plasmids of Yersinia pestis

JOURNAL J. Bacteriol. 180 (19), 5192-5202 (1998)

PUBMED 9748454

REFERENCE 2 (bases 1 to 100984)

AUTHORS Hu, P., Elliott, J., McCready, P., Skowronski, E., Garnes, J., Kobayashi, A., Carrano, A.V., Brubaker, R. and Garcia, E.

TITLE Direct Submission

JOURNAL Submitted (16-MAR-1998) Biology and Biotechnology Research, Lawrence Livermore National Lab, L452, 7000 East Ave., Livermore, CA 94550, USA

FEATURES Location/Qualifiers

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Best Local Similarity 100.0%; Pred. No. 7.2;
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RESULT 4
 AF053947/c

LOCUS AF053947 100984 bp DNA circular BCT 17-JUN-2003

DEFINITION Yersinia pestis KIM plasmid pMT1, complete sequence.

ACCESSION AF053947

VERSION AF053947.1 GI:2996286

KEYWORDS .

SOURCE Yersinia pestis KIM

ORGANISM Yersinia pestis KIM
 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 Enterobacteriaceae; Yersinia.

REFERENCE 1 (bases 1 to 100984)

AUTHORS Hu, P., Elliott, J., McCready, P., Skowronski, E., Garnes, J.,
 Kobayashi, A., Brubaker, R.R. and Garcia, E.

TITLE Structural organization of virulence-associated plasmids of
 Yersinia pestis

JOURNAL J. Bacteriol. 180 (19), 5192-5202 (1998)

PUBMED 9748454

REFERENCE 2 (bases 1 to 100984)

AUTHORS Hu, P., Elliott, J., McCready, P., Skowronski, E., Garnes, J.,
 Kobayashi, A., Carrano, A.V., Brubaker, R. and Garcia, E.

TITLE Direct Submission

JOURNAL Submitted (16-MAR-1998) Biology and Biotechnology Research,
 Lawrence Livermore National Lab, L452, 7000 East Ave., Livermore,
 CA 94550, USA

FEATURES Location/Qualifiers

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Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4
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LOCUS AF053947 100984 bp DNA circular BCT 17-JUN-2003

DEFINITION Yersinia pestis KIM plasmid pMT1, complete sequence.

ACCESSION AF053947

VERSION AF053947.1 GI:2996286

KEYWORDS .

SOURCE Yersinia pestis KIM

ORGANISM Yersinia pestis KIM

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Yersinia.

REFERENCE 1 (bases 1 to 100984)

AUTHORS Hu, P., Elliott, J., McCready, P., Skowronski, E., Garnes, J., Kobayashi, A., Brubaker, R.R. and Garcia, E.

TITLE Structural organization of virulence-associated plasmids of Yersinia pestis

JOURNAL J. Bacteriol. 180 (19), 5192-5202 (1998)

PUBMED 9748454

REFERENCE 2 (bases 1 to 100984)

AUTHORS Hu, P., Elliott, J., McCready, P., Skowronski, E., Garnes, J., Kobayashi, A., Carrano, A.V., Brubaker, R. and Garcia, E.

TITLE Direct Submission

JOURNAL Submitted (16-MAR-1998) Biology and Biotechnology Research, Lawrence Livermore National Lab, L452, 7000 East Ave., Livermore, CA 94550, USA

FEATURES Location/Qualifiers

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RESULT 3
 AF053947

LOCUS AF053947 100984 bp DNA circular BCT 17-JUN-2003

DEFINITION Yersinia pestis KIM plasmid pMT1, complete sequence.

ACCESSION AF053947

VERSION AF053947.1 GI:2996286

KEYWORDS .

SOURCE Yersinia pestis KIM

ORGANISM Yersinia pestis KIM

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Yersinia.

REFERENCE 1 (bases 1 to 100984)

AUTHORS Hu, P., Elliott, J., McCready, P., Skowronski, E., Garnes, J., Kobayashi, A., Brubaker, R.R. and Garcia, E.

TITLE Structural organization of virulence-associated plasmids of Yersinia pestis

JOURNAL J. Bacteriol. 180 (19), 5192-5202 (1998)

PUBMED 9748454

REFERENCE 2 (bases 1 to 100984)

AUTHORS Hu, P., Elliott, J., McCready, P., Skowronski, E., Garnes, J., Kobayashi, A., Carrano, A.V., Brubaker, R. and Garcia, E.

TITLE Direct Submission

JOURNAL Submitted (16-MAR-1998) Biology and Biotechnology Research, Lawrence Livermore National Lab, L452, 7000 East Ave., Livermore, CA 94550, USA

FEATURES Location/Qualifiers

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Query Match 100.0%; Score 147; DB 15; Length 100984;
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Bausch, Sarae

From: Bausch, Sarae
Sent: Thursday, June 29, 2006 2:57 PM
To: STIC-Biotech/ChemLib
Subject: 10/630536 nucleic acid search

Please do a standard nucleic acid sequence for the following: SEQ ID No. 1-8 of 10/630536.
Please print out the first 100 hits.

Thank you.

Sarae Bausch, Ph.D.
USPTO Art Unit 1634
REM 2 A 70
Mailbox: REM 2 C 70
(571) 272-2912

Tracking:	Recipient	Read
	STIC-Biotech/ChemLib	Read: 6/29/06 2:57 PM

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OM nucleic - nucleic search, using sw model

Run on: July 1, 2006, 04:17:07 ; Search time 1015.7 Seconds
(without alignments)
1541.534 Million cell updates/sec

Title: US-10-630-536-1
Perfect score: 28
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : EST:
1: gb_est1:
2: gb_est3:
3: gb_est4:
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5: gb_est6:
6: gb_htc:
7: gb_est2:
8: gb_est7:
9: gb_est8:
10: gb_est9:
11: gb_gss1:
12: gb_gss2:
13: gb_gss3:
14: gb_gss4:

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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Result	Query					Description
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c 2	20.6	73.6	375	14	AG254363	AG254363 Lotus cor
3	20.6	73.6	485	9	DR223685	DR223685 3175093 C
c 4	20.6	73.6	612	14	AG232848	AG232848 Lotus cor
c 5	20.6	73.6	875	12	CC657710	CC657710 OGDAG43TM
c 6	20.2	72.1	648	3	BU477783	BU477783 603844771
c 7	20	71.4	272	12	CG815211	CG815211 SOYEC63TV
8	20	71.4	417	1	AA176882	AA176882 zp10e05.r
9	20	71.4	488	4	BX495652	BX495652 DKFZp779G
c 10	20	71.4	501	1	AV523451	AV523451 AV523451
c 11	20	71.4	547	13	CL737451	CL737451 OR_BBa007
c 12	20	71.4	640	9	DN197183	DN197183 USDA-FP_1
c 13	20	71.4	711	13	CW664426	CW664426 OG_BBa001
c 14	20	71.4	724	13	CW662633	CW662633 OG_BBa001
c 15	20	71.4	828	13	CL821671	CL821671 OR_CBa004
c 16	20	71.4	843	3	BU750528	BU750528 CH3#034_A
17	20	71.4	868	13	CZ197785	CZ197785 AIAA-aag1
18	20	71.4	1180	2	BG847689	BG847689 1024018F1
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c 20	19.6	70.0	203	2	BF842384	BF842384 PM0-HT107
c 21	19.6	70.0	605	3	BQ388563	BQ388563 NISC_mq02
c 22	19.6	70.0	607	5	CF006669	CF006669 QBI21f12.
23	19.6	70.0	747	13	DU228816	DU228816 109857429
c 24	19.6	70.0	829	5	CF221759	CF221759 AGENCOURT
25	19.6	70.0	861	13	DU222493	DU222493 109857403
c 26	19.6	70.0	869	14	DU958392	DU958392 225547 To
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c 31	19.6	70.0	1501	12	CC263959	CC263959 CH261-184
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53	19.4	69.3	780	4	CB980281	CB980281 CAB70002_

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c 67	19.2	68.6	653	9	DN469148	DN469148 USDA-FP_1
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76	19.2	68.6	940	12	CG296976	CG296976 OG3BU83TH
77	19.2	68.6	1101	14	CNS00FPE	AL070880 Drosophil
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85	19	67.9	404	2	BJ934619	BJ934619 BJ934619
86	19	67.9	416	14	CT453068	CT453068 Sus scrof
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88	19	67.9	463	13	CZ298368	CZ298368 ZMMBF0069
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97	19	67.9	557	8	CV200481	CV200481 km04e08.y
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101	19	67.9	595	14	DE013378	DE013378 Branchios
102	19	67.9	596	10	DT280686	DT280686 JGI_CAAV9
103	19	67.9	613	10	DR638765	DR638765 EST102939
104	19	67.9	616	11	AZ605488	AZ605488 1M0426P18
105	19	67.9	625	5	CD319894	CD319894 StrPu538.
106	19	67.9	629	14	CR328767	CR328767 mtel-57N1
107	19	67.9	643	14	CR865642	CR865642 Sus scrof
108	19	67.9	645	2	BM489526	BM489526 pgm2n.pk0
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112	19	67.9	681	14	DU749312	DU749312 HF10_110_
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c 115	19	67.9	694	7	BF031627	BF031627 601558107
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c 117	19	67.9	707	9	CX577937	CX577937 TTE000321
c 118	19	67.9	708	11	BZ148827	BZ148827 CH230-395
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121	19	67.9	724	12	CL188575	CL188575 104_405_1
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127	19	67.9	780	14	CR268915	CR268915 Reverse s
128	19	67.9	783	14	CNS07BMA	AL438056 T7 end of
c 129	19	67.9	786	3	BQ150215	BQ150215 NF012G09L
130	19	67.9	790	12	CG092006	CG092006 PUFKH44TD
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c 132	19	67.9	804	5	CJ445574	CJ445574 CJ445574
133	19	67.9	806	14	AJ595292	AJ595292 Arabidops
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136	19	67.9	810	4	BX079454	BX079454 BX079454
137	19	67.9	812	4	CA920739	CA920739 EST638457
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c 139	19	67.9	812	13	DU050592	DU050592 145226 To
c 140	19	67.9	814	8	CV289966	CV289966 aof01-11m
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c 142	19	67.9	822	13	CZ953200	CZ953200 265024 To
c 143	19	67.9	824	11	B12075	B12075 F25H9-Sp6.2
144	19	67.9	826	8	CO421648	CO421648 GGEZHT102
c 145	19	67.9	849	14	DU870776	DU870776 101855 To
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c 147	19	67.9	865	8	CV771138	CV771138 FGAS06553
c 148	19	67.9	880	13	CZ970396	CZ970396 174110 To
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ALIGNMENTS

RESULT 1
AG889518/c

LOCUS AG889518 912 bp DNA linear GSS 03-NOV-2004

DEFINITION Oryza sativa (indica cultivar-group) genomic DNA, BAC end sequence, BAC clone:K0359C09_F, genomic survey sequence.

ACCESSION AG889518

VERSION AG889518.1 GI:55355779

KEYWORDS GSS.

SOURCE Oryza sativa (indica cultivar-group)

ORGANISM Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1

AUTHORS Katagiri,S., Wu,J., Ito,Y., Karasawa,W., Shibata,M., Kanamori,H., Katayose,Y., Namiki,N., Matsumoto,T. and Sasaki,T.

TITLE End Sequencing and Chromosomal in silico Mapping of BAC Clones Derived from an indica Rice Cultivar, Kasalath

JOURNAL Breeding Science 54, 273-279 (2004)

REFERENCE 2 (bases 1 to 912)

SCORE Search Results Details for Application 10630-536-2.rge

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OM nucleic - nucleic search, using sw model

Run on: July 1, 2006, 03:55:42 ; Search time 417.254 Seconds
 (without alignments)
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Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

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 Listing first 150 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c 4	28	100.0	96210	15	YPPMT1		AL117211 Yersinia
5	28	100.0	100984	15	AF053947		AF053947 Yersinia
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c 11	21.2	75.7	277211	12	AC164850		AC164850 Bos tauru
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c 13	20.6	73.6	110000	4	AY661558_0		AY661558 Hordeum v
14	20.6	73.6	138587	5	AC010363		AC010363 Homo sapi
c 15	20.6	73.6	143009	5	AC022447		AC022447 Homo sapi
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c 18	20.6	73.6	250440	12	AC095968		AC095968 Rattus no
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23	20	71.4	589	7	BV356900		BV356900 S231P6154
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c 42	19.8	70.7	4122	2	CQ574715		CQ574715 Sequence
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c 44	19.8	70.7	81329	12	AC008300		AC008300 Drosophil
c 45	19.8	70.7	156346	13	AC006472		AC006472 Drosophil
46	19.8	70.7	162995	6	AL663032		AL663032 Mouse DNA
c 47	19.8	70.7	186241	13	AC007086		AC007086 Drosophil
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49	19.8	70.7	297107	13	AE003833		AE003833 Drosophil
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c 51	19.6	70.0	77850	5	AC080098		AC080098 Homo sapi
52	19.6	70.0	92527	12	AC144962		AC144962 Xenopus t
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c 54	19.6	70.0	128449	12	AC148508		AC148508 Carollia
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c 56	19.6	70.0	143714	5	AL390856		AL390856 Human DNA

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c 64	19.6	70.0	243184	12	AC103523	AC103523 Rattus no
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116	19	67.9	86797	12	AP008129	AP008129 Lotus cor
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c 147	19	67.9	150446	12	CT030221	CT030221 Danio rer
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ALIGNMENTS

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 ACCESSION CS001821
 VERSION CS001821.1 GI:58424076
 KEYWORDS .
 SOURCE Yersinia pestis
 ORGANISM Yersinia pestis
 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 Enterobacteriaceae; Yersinia.
 REFERENCE 1
 AUTHORS McCready, P.M., Radnedge, L., Andersen, G.L., Ott, L.L., Slezak, T.R.,
 Kuczmarski, T.A. and Motin, V.L.
 TITLE Nucleotide sequences specific to Yersinia pestis and methods for
 the detection of Yersinia pestis
 JOURNAL Patent: WO 2004106553-A 2 09-DEC-2004;
 The Regents of The University of California (US)
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OM nucleic - nucleic search, using sw model

Run on: July 1, 2006, 03:53:57 ; Search time 168.804 Seconds
(without alignments)
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Title: US-10-630-536-1

Perfect score: 28

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Gapop 10.0 , Gapext 1.0

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SUMMARIES

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	37	18	64.3	300	13	ADV85435	Adv85435 Streptoco
c	38	18	64.3	398	6	ABL88717	Abl88717 Conus bet
c	39	18	64.3	418	6	ABL88712	Abl88712 Conus bet
c	40	18	64.3	423	6	ABL88716	Abl88716 Conus bet
c	41	18	64.3	423	6	ABL88711	Abl88711 Conus bet
c	42	18	64.3	424	6	ABL88714	Abl88714 Conus bet
c	43	18	64.3	424	6	ABL88710	Abl88710 Conus bet
c	44	18	64.3	424	6	ABL88713	Abl88713 Conus bet
c	45	18	64.3	516	6	ABZ16785	Abz16785 Arabidops
	46	18	64.3	591	5	ABV59140	Abv59140 Human pro
	47	18	64.3	771	10	ADH84839	Adh84839 Enterococ
	48	18	64.3	825	10	ADF00371	Adf00371 Bacterial
	49	18	64.3	1772	12	ADQ63378	Adq63378 Novel hum
c	50	18	64.3	1926	8	ABT21011	Abt21011 Aspergill
c	51	18	64.3	2000	8	ADA71468	Ada71468 Rice gene
c	52	18	64.3	2137	8	ABT18597	Abt18597 Aspergill
	53	18	64.3	2393	13	ADX45974	Adx45974 Plant ful
c	54	18	64.3	2451	8	ABT20413	Abt20413 Aspergill
	55	18	64.3	2494	6	ABN85763	Abn85763 Maize yel
	56	18	64.3	2582	13	ADX46627	Adx46627 Plant ful

57	18	64.3	2630	4	ABL14403	Abl14403 Drosophil
c 58	18	64.3	4136	8	ABT18003	Abt18003 Aspergill
c 59	18	64.3	4451	8	ABT19817	Abt19817 Aspergill
60	18	64.3	4496	13	ADR31301	Adr31301 Aspergill
61	18	64.3	4892	4	ABL14402	Abl14402 Drosophil
c 62	18	64.3	13837	4	ABL16716	Abl16716 Drosophil
63	18	64.3	14416	4	ABL14206	Abl14206 Drosophil
c 64	18	64.3	20356	13	ADV87713	Adv87713 Streptoco
c 65	18	64.3	20356	13	ADV78966	Adv78966 Streptoco
66	18	64.3	25599	4	ABL16668	Abl16668 Drosophil
c 67	18	64.3	110000	13	ADV81204_11	Continuation (12 o
c 68	18	64.3	176001	12	ADK43203	Adk43203 Human pro
c 69	18	64.3	186739	12	ADK43195	Adk43195 Human pro
c 70	17.6	62.9	1477	3	AAC39037	Aac39037 Arabidops
c 71	17.6	62.9	2328	15	AEF55829	Aef55829 Human gen
72	17.6	62.9	3217	12	ADQ64499	Adq64499 Novel hum
73	17.6	62.9	5265	14	AEA12645	Aea12645 DNA encod
c 74	17.6	62.9	5474	6	ABL33041	Abl33041 Human imm
c 75	17.6	62.9	5474	6	ABQ66992	Abq66992 Human ang
76	17.6	62.9	8858	2	AAZ10202	Aaz10202 Expressio
77	17.6	62.9	8858	6	AAH43777	Aah43777 Chi220 li
78	17.6	62.9	8858	14	ADV85636	Adv85636 Anti-huma
79	17.6	62.9	8874	12	ADJ65027	Adj65027 Plasmid p
80	17.6	62.9	8897	2	AAV18692	Aav18692 Plasmid p
81	17.6	62.9	8897	2	AAV18693	Aav18693 Plasmid p
82	17.6	62.9	9362	6	ABV72729	Abv72729 Expressio
83	17.6	62.9	9362	14	ADY80266	Ady80266 Nucleotid
84	17.6	62.9	9400	6	ABV72728	Abv72728 Expressio
85	17.6	62.9	9400	14	ADY80265	Ady80265 Nucleotid
86	17.6	62.9	13615	8	ACD26275	Acd26275 Nasophary
c 87	17.6	62.9	37373	14	AEC76962	Aec76962 Bacillus
c 88	17.6	62.9	40869	14	AEC76963	Aec76963 Bacillus
c 89	17.6	62.9	75384	4	AAK85590	Aak85590 Human imm
c 90	17.6	62.9	107622	14	AEE04904	Aee04904 Cancer-as
91	17.6	62.9	110000	14	AEB42401_13	Continuation (14 o
c 92	17.6	62.9	262090	12	ADQ59207	Adq59207 MSI-H car
93	17.4	62.1	111	4	AAI23835	Aai23835 Probe #13
94	17.4	62.1	111	4	ABA68953	Aba68953 Human foe
95	17.4	62.1	111	4	AAI49148	Aai49148 Probe #17
96	17.4	62.1	111	4	ABA50972	Aba50972 Human bre
97	17.4	62.1	111	4	ABA35902	Aba35902 Probe #14
98	17.4	62.1	111	4	AAK43071	Aak43071 Human bon
99	17.4	62.1	111	4	AAK17281	Aak17281 Human bra
100	17.4	62.1	111	4	ABS42706	Abs42706 Human liv
101	17.4	62.1	111	5	AAI09442	Aai09442 Probe #94
102	17.4	62.1	111	6	ABS17140	Abs17140 Human gen
103	17.4	62.1	121	10	ADH92454	Adh92454 Human gen
c 104	17.4	62.1	159	12	ADH00216	Adh00216 Kidney di
105	17.4	62.1	326	6	ABN94321	Abn94321 Gene #819
106	17.4	62.1	354	4	AAI14641	Aai14641 Probe #45
107	17.4	62.1	354	4	ABA56371	Aba56371 Human foe
108	17.4	62.1	354	4	AAI36013	Aai36013 Probe #46
109	17.4	62.1	354	4	ABA45854	Aba45854 Human bre
110	17.4	62.1	354	4	ABA26008	Aba26008 Probe #44
111	17.4	62.1	354	4	AAK30050	Aak30050 Human bon
112	17.4	62.1	354	4	AAK04546	Aak04546 Human bra
113	17.4	62.1	354	4	ABS29701	Abs29701 Human liv
114	17.4	62.1	354	5	AAI04452	Aai04452 Probe #44
115	17.4	62.1	354	6	ABS04624	Abs04624 Human gen
c 116	17.4	62.1	380	4	AAK80718	Aak80718 Human imm
117	17.4	62.1	415	4	AAK62055	Aak62055 Human imm

SCORE Search Results Details for Application 10630536 and Search Result us-10-630-536-1.i

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This page gives you Search Results detail for the Application 10630536 and Search Result us-10-630-536-1.i.rni.

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OM nucleic - nucleic search, using sw model

Run on: July 1, 2006, 04:28:37 ; Search time 34.3636 Seconds
(without alignments)
1524.607 Million cell updates/sec

Title: US-10-630-536-1

Perfect score: 28

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : Issued_Patents_NA:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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					Description

c	1	28	100.0	100990	3	US-09-409-800B-2	Sequence 2, Appli
	2	18.4	65.7	251769	3	US-09-949-016-13185	Sequence 13185, A
	3	18.4	65.7	251769	3	US-09-949-016-13186	Sequence 13186, A
	4	18.4	65.7	266748	3	US-09-949-016-13187	Sequence 13187, A
	5	18.4	65.7	266748	3	US-09-949-016-13188	Sequence 13188, A
c	6	18.4	65.7	1082144	4	US-09-531-120-211	Sequence 211, App
	7	18	64.3	332	3	US-09-270-767-31470	Sequence 31470, A
c	8	18	64.3	398	3	US-09-894-882-175	Sequence 175, App
c	9	18	64.3	418	3	US-09-894-882-160	Sequence 160, App
c	10	18	64.3	423	3	US-09-894-882-157	Sequence 157, App
c	11	18	64.3	423	3	US-09-894-882-172	Sequence 172, App
c	12	18	64.3	424	3	US-09-894-882-154	Sequence 154, App
c	13	18	64.3	424	3	US-09-894-882-163	Sequence 163, App
c	14	18	64.3	424	3	US-09-894-882-166	Sequence 166, App
	15	18	64.3	771	3	US-09-134-000C-2724	Sequence 2724, Ap
	16	18	64.3	825	3	US-09-543-681A-656	Sequence 656, App
	17	18	64.3	902	3	US-09-270-767-15151	Sequence 15151, A
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c	19	18	64.3	56665	3	US-09-949-016-14026	Sequence 14026, A
	20	17.6	62.9	8858	3	US-09-247-352-6	Sequence 6, Appli
	21	17.6	62.9	8858	3	US-09-466-635-6	Sequence 6, Appli
	22	17.6	62.9	8874	3	US-10-630-406-6	Sequence 6, Appli
c	23	17.6	62.9	76610	3	US-09-949-016-15521	Sequence 15521, A
c	24	17.6	62.9	235064	3	US-09-949-016-15390	Sequence 15390, A
	25	17.4	62.1	326	4	US-09-880-107-819	Sequence 819, App
	26	17.4	62.1	601	3	US-09-949-016-24637	Sequence 24637, A
	27	17.4	62.1	601	3	US-09-949-016-36215	Sequence 36215, A
	28	17.4	62.1	601	3	US-09-949-016-158579	Sequence 158579,
	29	17.4	62.1	601	3	US-09-949-016-158583	Sequence 158583,
	30	17.4	62.1	601	3	US-09-949-016-158587	Sequence 158587,
	31	17.4	62.1	601	3	US-09-949-016-158591	Sequence 158591,
	32	17.4	62.1	601	3	US-09-949-016-206267	Sequence 206267,
c	33	17.4	62.1	601	3	US-09-949-002-3237	Sequence 3237, Ap
c	34	17.4	62.1	601	3	US-09-949-002-3238	Sequence 3238, Ap
c	35	17.4	62.1	601	3	US-09-949-002-7321	Sequence 7321, Ap
c	36	17.4	62.1	601	3	US-09-949-002-7322	Sequence 7322, Ap
	37	17.4	62.1	603	3	US-09-248-796A-9942	Sequence 9942, Ap
c	38	17.4	62.1	717	3	US-08-998-416-667	Sequence 667, App
c	39	17.4	62.1	781	3	US-09-533-559-5861	Sequence 5861, Ap
c	40	17.4	62.1	840	3	US-09-248-796A-6353	Sequence 6353, Ap
	41	17.4	62.1	1271	3	US-09-949-016-931	Sequence 931, App
	42	17.4	62.1	1271	5	US-10-131-831-9112	Sequence 9112, Ap
	43	17.4	62.1	1279	3	US-09-949-016-4430	Sequence 4430, Ap
	44	17.4	62.1	1279	3	US-09-949-016-4431	Sequence 4431, Ap
	45	17.4	62.1	1364	3	US-09-949-016-329	Sequence 329, App
	46	17.4	62.1	1372	3	US-09-949-016-4432	Sequence 4432, Ap
	47	17.4	62.1	1372	3	US-09-949-016-4433	Sequence 4433, Ap
	48	17.4	62.1	1415	3	US-09-914-098-57	Sequence 57, Appl
	49	17.4	62.1	1560	3	US-09-540-236-1130	Sequence 1130, Ap
c	50	17.4	62.1	1797	3	US-09-248-796A-5087	Sequence 5087, Ap
	51	17.4	62.1	2310	3	US-09-248-796A-4162	Sequence 4162, Ap
	52	17.4	62.1	11543	3	US-09-949-016-12071	Sequence 12071, A
	53	17.4	62.1	11543	3	US-09-949-016-12673	Sequence 12673, A
	54	17.4	62.1	11544	3	US-09-949-016-16172	Sequence 16172, A
	55	17.4	62.1	11544	3	US-09-949-016-16173	Sequence 16173, A
	56	17.4	62.1	11544	3	US-09-949-016-16174	Sequence 16174, A
	57	17.4	62.1	11544	3	US-09-949-016-16175	Sequence 16175, A
c	58	17.4	62.1	29037	3	US-09-949-016-14131	Sequence 14131, A
	59	17.4	62.1	33778	3	US-09-596-002-19	Sequence 19, Appl
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c	61	17.4	62.1	51723	3	US-09-949-016-12152	Sequence 12152, A
c	62	17.4	62.1	51723	3	US-09-949-016-16991	Sequence 16991, A
c	63	17.4	62.1	91831	3	US-09-949-016-13694	Sequence 13694, A
	64	17.4	62.1	94987	3	US-09-949-016-12510	Sequence 12510, A
c	65	17.4	62.1	105045	3	US-09-949-002-663	Sequence 663, App
c	66	17.4	62.1	107045	3	US-09-949-002-772	Sequence 772, App
c	67	17.4	62.1	116955	3	US-09-949-016-17565	Sequence 17565, A
c	68	17.4	62.1	124110	3	US-09-949-016-13353	Sequence 13353, A
c	69	17.4	62.1	222452	3	US-09-949-016-12968	Sequence 12968, A
c	70	17.4	62.1	611587	4	US-09-531-120-209	Sequence 209, App
	71	17.4	62.1	640681	3	US-09-790-988-1	Sequence 1, Appli
c	72	17.4	62.1	786431	3	US-09-751-389-3	Sequence 3, Appli
	73	17.4	62.1	1230025	3	US-09-198-452A-1	Sequence 1, Appli
	74	17.4	62.1	1230230	3	US-09-438-185A-1	Sequence 1, Appli
c	75	17.2	61.4	366	3	US-09-248-796A-4875	Sequence 4875, Ap
c	76	17.2	61.4	7120	3	US-09-380-773-2	Sequence 2, Appli
	77	17	60.7	492	3	US-09-328-352-1653	Sequence 1653, Ap
	78	17	60.7	601	3	US-09-949-016-185602	Sequence 185602,
	79	17	60.7	627	3	US-09-533-559-6577	Sequence 6577, Ap
	80	17	60.7	2384	3	US-09-894-912A-31	Sequence 31, Appl
	81	17	60.7	4819	3	US-09-774-528-72	Sequence 72, Appl
	82	17	60.7	4819	3	US-10-120-988-72	Sequence 72, Appl
c	83	17	60.7	16011	3	US-09-600-319-3	Sequence 3, Appli
c	84	17	60.7	16011	3	US-10-057-726-16	Sequence 16, Appl
	85	17	60.7	80246	3	US-09-078-294-4	Sequence 4, Appli
	86	17	60.7	80595	3	US-09-078-294-3	Sequence 3, Appli
	87	17	60.7	101349	3	US-09-949-016-17433	Sequence 17433, A
c	88	17	60.7	113966	3	US-09-949-016-12277	Sequence 12277, A
c	89	17	60.7	113967	3	US-09-949-016-17051	Sequence 17051, A
c	90	17	60.7	160759	3	US-09-949-016-16514	Sequence 16514, A
	91	17	60.7	4403765	3	US-09-103-840A-2	Sequence 2, Appli
	92	17	60.7	4411529	3	US-09-103-840A-1	Sequence 1, Appli
	93	16.8	60.0	153	2	US-08-188-228-37	Sequence 37, Appl
	94	16.8	60.0	153	2	US-08-332-643-37	Sequence 37, Appl
	95	16.8	60.0	153	2	US-08-332-638-37	Sequence 37, Appl
	96	16.8	60.0	225	3	US-09-248-796A-9858	Sequence 9858, Ap
c	97	16.8	60.0	483	3	US-09-248-796A-2679	Sequence 2679, Ap
	98	16.8	60.0	601	3	US-09-949-016-48044	Sequence 48044, A
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	107	16.8	60.0	1422	3	US-09-248-796A-5892	Sequence 5892, Ap
c	108	16.8	60.0	1704	3	US-09-328-352-1786	Sequence 1786, Ap
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	110	16.8	60.0	2490	2	US-08-188-228-45	Sequence 45, Appl
	111	16.8	60.0	2490	2	US-08-332-638-45	Sequence 45, Appl
	112	16.8	60.0	2646	3	US-09-614-221A-366	Sequence 366, App
c	113	16.8	60.0	2673	3	US-09-519-232-73	Sequence 73, Appl
	114	16.8	60.0	22067	3	US-09-820-001-3	Sequence 3, Appli
	115	16.8	60.0	22067	3	US-10-003-302-3	Sequence 3, Appli
	116	16.8	60.0	26075	3	US-09-949-016-12004	Sequence 12004, A
	117	16.8	60.0	26076	3	US-09-949-016-13041	Sequence 13041, A
	118	16.8	60.0	52711	3	US-09-949-016-12224	Sequence 12224, A
	119	16.8	60.0	52865	3	US-09-949-016-15618	Sequence 15618, A
	120	16.8	60.0	58543	3	US-09-949-016-13565	Sequence 13565, A
	121	16.8	60.0	62474	3	US-09-949-016-15182	Sequence 15182, A

SCORE Search Results Details for Application 10630536 and Search Result us-10-630-536-1.rnpbn.

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OM nucleic - nucleic search, using sw model

Run on: July 1, 2006, 04:39:12 ; Search time 29.0718 Seconds
(without alignments)
1138.902 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 1619540

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	19.2	68.6	909203	7	US-11-266-748A-29039	Sequence 29039, A
c 3	18.6	66.4	664	7	US-11-266-748A-169847	Sequence 169847,
	18.6	66.4	664	7	US-11-266-748A-244959	Sequence 244959,
c 5	18.6	66.4	2609	6	US-10-449-902-22882	Sequence 22882, A
	18.4	65.7	1272	7	US-11-217-529-3057	Sequence 3057, Ap
	18.4	65.7	1828	6	US-10-449-902-9749	Sequence 9749, Ap
c 8	18.2	65.0	2954	6	US-10-449-902-10055	Sequence 10055, A
c 9	18	64.3	1000	7	US-11-266-748A-204417	Sequence 204417,
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ALIGNMENTS

RESULT 1

US-10-449-902-13585/c

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; Sequence 13585, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13585
; LENGTH: 816
; TYPE: DNA
; ORGANISM: Oryza sativa
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK110933
; DATABASE ENTRY DATE: 2001-12-06

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SCORE Search Results Details for Application 10630536 and Search Result us-10-630-536-2.rng.

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Title: US-10-630-536-2

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SUMMARIES

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83	17.6	62.9	190	4	ABS42469	Abs42469 Human liv
84	17.6	62.9	190	5	AAI09216	Aai09216 Probe #92
85	17.6	62.9	190	6	ABS16893	Abs16893 Human gen
86	17.6	62.9	245	12	ADO34646	Ado34646 Human SLI
c 87	17.6	62.9	454	13	ADX46463	Adx46463 Plant ful
88	17.6	62.9	463	4	AAI14400	Aai14400 Probe #43
89	17.6	62.9	463	4	ABA56127	Aba56127 Human foe
90	17.6	62.9	463	4	AAI35773	Aai35773 Probe #44
91	17.6	62.9	463	4	ABA45622	Aba45622 Human bre
92	17.6	62.9	463	4	ABA25778	Aba25778 Probe #42
93	17.6	62.9	463	4	AAK29811	Aak29811 Human bon
94	17.6	62.9	463	4	AAK04315	Aak04315 Human bra
95	17.6	62.9	463	4	ABS29459	Abs29459 Human liv
96	17.6	62.9	463	5	AAI04223	Aai04223 Probe #42
97	17.6	62.9	463	6	ABS04371	Abs04371 Human gen
c 98	17.6	62.9	660	6	ABN93342	Abn93342 Staphyloc
c 99	17.6	62.9	660	13	ADS04351	Ads04351 Staphyloc
c 100	17.6	62.9	685	8	ACA22764	Aca22764 Prokaryot
c 101	17.6	62.9	985	8	ACA22689	Aca22689 Prokaryot
102	17.6	62.9	1479	14	ADW07606	Adw07606 GTase cDN
c 103	17.6	62.9	1807	3	AAC51305	Aac51305 Arabidops
c 104	17.6	62.9	1812	3	AAC39116	Aac39116 Arabidops
c 105	17.6	62.9	1963	10	ADG10825	Adg10825 Human STA
106	17.6	62.9	2000	11	ACL38016	Acl38016 Rice stre
c 107	17.6	62.9	2496	13	ADX51760	Adx51760 Plant ful
c 108	17.6	62.9	2640	13	ADX49949	Adx49949 Plant ful
c 109	17.6	62.9	2737	13	ADX36444	Adx36444 Plant ful
110	17.6	62.9	3182	4	AAH54683	Aah54683 S. epider
111	17.6	62.9	3618	4	AAH54200	Aah54200 S. epider
c 112	17.6	62.9	4905	13	ADR23438	Adr23438 Fatty acy
c 113	17.6	62.9	5024	10	ADG10713	Adg10713 Human STA
c 114	17.6	62.9	5033	12	ADL12412	Adl12412 Human ste
c 115	17.6	62.9	5043	12	ADJ45488	Adj45488 cDNA enco
c 116	17.6	62.9	5043	12	ADP05440	Adp05440 Human ace
c 117	17.6	62.9	5043	12	ADQ79557	Adq79557 Human hep

c 118	17.6	62.9	5043	13	ADR25183	Adr25183 Breast ca
c 119	17.6	62.9	5043	13	ADR23436	Adr23436 Fatty acy
c 120	17.6	62.9	5043	13	ACF91619	Acf91619 Human SIR
c 121	17.6	62.9	5043	15	AEF74530	Aef74530 Human pol
c 122	17.6	62.9	5336	10	ADG10715	Adg10715 Human STA
c 123	17.6	62.9	5356	9	ACF04122	Acf04122 Human Fac
c 124	17.6	62.9	5356	13	ADR23437	Adr23437 Fatty acy
c 125	17.6	62.9	5356	13	ACF91620	Acf91620 Human SIR
c 126	17.6	62.9	5356	14	AED14396	Aed14396 Human cum
127	17.6	62.9	10593	14	ACL64567	Acl64567 M. xanthu
128	17.6	62.9	39159	4	ABL30024	Ab130024 Drosophil
c 129	17.6	62.9	39536	4	ABL15482	Ab115482 Drosophil
c 130	17.6	62.9	59359	11	ACN44220	Acn44220 Mouse gen
131	17.6	62.9	110000	12	ADO34435_4	Continuation (5 of
132	17.6	62.9	110000	12	ADO34435_5	Continuation (6 of
c 133	17.6	62.9	127432	12	ADO43653	Ado43653 Nucleotid
c 134	17.6	62.9	138941	8	ACC79695	Acc79695 Human tum
135	17.4	62.1	114	12	ADL10463	Adl10463 Cat flea
136	17.4	62.1	117	12	ADL11274	Adl11274 Cat flea
c 137	17.4	62.1	118	3	AAC94432	Aac94432 Cat flea
c 138	17.4	62.1	118	12	ADL11144	Adl11144 Cat flea
c 139	17.4	62.1	118	12	ADL11471	Adl111471 Cat flea
140	17.4	62.1	118	12	ADL10038	Adl10038 Cat flea
c 141	17.4	62.1	118	12	ADL10921	Adl10921 Cat flea
142	17.4	62.1	118	12	ADL11480	Adl111480 Cat flea
143	17.4	62.1	118	12	ADL10804	Adl10804 Cat flea
c 144	17.4	62.1	118	12	ADL09955	Adl09955 Cat flea
145	17.4	62.1	118	12	ADL10065	Adl10065 Cat flea
c 146	17.4	62.1	118	12	ADL11375	Adl111375 Cat flea
147	17.4	62.1	118	12	ADL10089	Adl10089 Cat flea
c 148	17.4	62.1	118	12	ADL11037	Adl111037 Cat flea
149	17.4	62.1	118	12	ADL11411	Adl111411 Cat flea
c 150	17.4	62.1	119	12	ADL10000	Adl10000 Cat flea

ALIGNMENTS

RESULT 1

ADV04867

ID ADV04867 standard; DNA; 28 BP.

XX

AC ADV04867;

XX

DT 24-FEB-2005 (first entry)

XX

DE Yersinia pestis amplicon #1 reverse PCR primer.

XX

KW Diagnosis; gene amplification; yersinia pestis infection; ss; PCR;
KW primer.

XX

OS Yersinia pestis.

XX

PN WO2004106553-A2.

XX

PD 09-DEC-2004.

XX

PF 31-JUL-2003; 2003WO-US024135.

XX

PR 01-AUG-2002; 2002US-0400890P.

PR 29-JUL-2003; 2003US-00400890.

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OM nucleic - nucleic search, using sw model

Run on: July 1, 2006, 04:28:37 ; Search time 34.3636 Seconds
(without alignments)
1524.607 Million cell updates/sec

Title: US-10-630-536-2

Perfect score: 28

Sequence: 1 ccatgttcatgttatgtccaccaacaag 28

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
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10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result %
Query

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c	3	19	67.9	884	3 US-09-042-225-3 Sequence 3, Appli
c	4	18.6	66.4	1353	3 US-09-489-039A-2881 Sequence 2881, Ap
c	5	18.4	65.7	441	3 US-09-270-767-4147 Sequence 4147, Ap
c	6	18.4	65.7	441	3 US-09-270-767-19429 Sequence 19429, A
c	7	18.4	65.7	798	3 US-09-248-796A-6709 Sequence 6709, Ap
c	8	18.4	65.7	900	2 US-08-181-271A-4 Sequence 4, Appli
c	9	18.4	65.7	900	2 US-08-449-315-4 Sequence 4, Appli
c	10	18.4	65.7	900	2 US-08-444-803-4 Sequence 4, Appli
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c	14	18.4	65.7	900	2 US-08-455-244-4 Sequence 4, Appli
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c	16	18.4	65.7	900	2 US-08-457-364-4 Sequence 4, Appli
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c	19	18.4	65.7	900	2 US-08-455-736-4 Sequence 4, Appli
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	24	18.4	65.7	2608	3 US-10-104-047-1057 Sequence 1057, Ap
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	37	18	64.3	18556	3 US-09-949-016-15177 Sequence 15177, A
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	39	18	64.3	99500	3 US-09-798-096-10 Sequence 10, Appli
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	43	17.6	62.9	601	3 US-09-949-016-109300 Sequence 109300,
	44	17.6	62.9	601	3 US-09-949-016-109301 Sequence 109301,
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	46	17.6	62.9	1230	3 US-09-248-796A-1393 Sequence 1393, Ap
	47	17.6	62.9	3182	3 US-09-710-279-4047 Sequence 4047, Ap
	48	17.6	62.9	3618	3 US-09-710-279-3564 Sequence 3564, Ap
c	49	17.6	62.9	4943	3 US-09-949-016-1397 Sequence 1397, Ap
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	51	17.6	62.9	10593	3 US-09-902-540-1030 Sequence 1030, Ap
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	59	17.4	62.1	1123	3 US-09-894-698-9 Sequence 9, Appli

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	76	17.4	62.1	89268	3	US-09-949-016-12025	Sequence 12025, A
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c	111	17	60.7	2770	3	US-09-977-261-5	Sequence 5, Appli
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c	120	17	60.7	4134	3	US-10-270-795-17	Sequence 17, Appli

c 121	17	60.7	4134	3	US-10-270-876-17	Sequence 17, Appl
c 122	17	60.7	4134	3	US-10-268-051-7	Sequence 7, Appli
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ALIGNMENTS

RESULT 1

US-09-409-800B-2
; Sequence 2, Application US/09409800B
; Patent No. 6706522
; GENERAL INFORMATION:
; APPLICANT: Blattner, Frederick R.
; APPLICANT: Burland, Valerie
; APPLICANT: Rose, Debra J.
; APPLICANT: Mayhew, George F.
; APPLICANT: Perna, Nicole
; APPLICANT: Perry, Robert D.
; APPLICANT: Straley, Susan C.
; APPLICANT: Fetherston, Jacqueline D.
; APPLICANT: Lindler, Luther E.
; APPLICANT: Plano, Gregory V.
; TITLE OF INVENTION: Plasmid DNA From Yersinia Pestis
; FILE REFERENCE: 960296.95939
; CURRENT APPLICATION NUMBER: US/09/409,800B
; CURRENT FILING DATE: 1999-09-30
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 100990
; TYPE: DNA
; ORGANISM: Yersinia pestis
US-09-409-800B-2

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OM nucleic - nucleic search, using sw model

Run on: July 1, 2006, 04:38:10 ; Search time 389.789 Seconds
(without alignments)
882.666 Million cell updates/sec

Title: US-10-630-536-2

Perfect score: 28

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Scoring table: IDENTITY_NUC
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Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

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ALIGNMENTS

RESULT 1

US-10-630-536-2

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; Publication No. US20060019254A1
; GENERAL INFORMATION:
; APPLICANT: McCready, Paula M
; APPLICANT: Radnedge, Lyndsay
; APPLICANT: Anderson, Gary L.
; APPLICANT: Ott, Linda L.
; APPLICANT: Slezak, Thomas R.
; APPLICANT: Kuczmarski, Thomas A.
; APPLICANT: Motin, Vladimir L.
; TITLE OF INVENTION: Nucleotide Sequences Specific to Yersinia Pestis and Methods fo
; TITLE OF INVENTION: Detection of Yersinia Pestis
; FILE REFERENCE: IL-11030
; CURRENT APPLICATION NUMBER: US/10/630,536
; CURRENT FILING DATE: 2003-07-29
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
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SCORE Search Results Details for Application 1

Search Result us-10-630-536-2.rnpl

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This page gives you Search Results detail for the Application 10630536 and Search Result us-10-6:
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c 135	16.4	58.6	1547	7	US-11-266-748A-251033	Sequence 251033,
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ALIGNMENTS

RESULT 1

US-11-266-748A-23957

; Sequence 23957, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996

SCORE Search Results Details for Application 10630536 and Search Result us-10-630-536-2.rst.

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(without alignments)
1541.534 Million cell updates/sec

Title: US-10-630-536-2
Perfect score: 28
Sequence: 1 ccatgttcatgttatgtccaccaacaag 28

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : EST:
1: gb_est1:
2: gb_est3:
3: gb_est4:
4: gb_est5:
5: gb_est6:
6: gb_htc:
7: gb_est2:
8: gb_est7:
9: gb_est8:
10: gb_est9:
11: gb_gss1:
12: gb_gss2:
13: gb_gss3:
14: gb_gss4:

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

%

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c 124	19	67.9	595	13	CW059671	CW059671 104_302_1
125	19	67.9	601	3	BQ147300	BQ147300 NF038H06F
126	19	67.9	606	2	BJ463811	BJ463811 BJ463811
127	19	67.9	606	10	DT700345	DT700345 s13dFA29F
128	19	67.9	610	7	AV940730	AV940730 AV940730
129	19	67.9	611	10	DT708137	DT708137 s13dFA27C
c 130	19	67.9	612	10	DT707031	DT707031 s13dFA09H
131	19	67.9	615	10	DT712983	DT712983 s13dFA19G
132	19	67.9	616	4	CB860990	CB860990 HH03L24w
133	19	67.9	621	10	DT670043	DT670043 s13dLT30F
c 134	19	67.9	624	6	CNS0A9BK	BX821982 Arabidops
135	19	67.9	627	10	DT713664	DT713664 s13dFA32A
136	19	67.9	630	10	DW072797	DW072797 CLLZ4204.
137	19	67.9	631	2	BM443573	BM443573 EBro02_SQ
c 138	19	67.9	632	4	CA007979	CA007979 HU09I22r
139	19	67.9	633	10	DW060231	DW060231 CLLY12767
140	19	67.9	638	10	DW050751	DW050751 CLLX3537.
141	19	67.9	641	10	DW072683	DW072683 CLLZ410.b
142	19	67.9	642	10	DT711827	DT711827 s13dFA22D
143	19	67.9	642	10	DW048821	DW048821 CLLX1567.
144	19	67.9	642	10	DW050755	DW050755 CLLX3541.
145	19	67.9	648	2	BI960398	BI960398 HVSMEn002
c 146	19	67.9	648	13	CL747853	CL747853 OR_BBa011
147	19	67.9	649	10	DW069772	DW069772 CLLY9589.
148	19	67.9	649	10	DW070831	DW070831 CLLZ2207.
c 149	19	67.9	650	2	BG711605	BG711605 pg11n.pk0
150	19	67.9	651	5	CK450482	CK450482 900039 MA

ALIGNMENTS

RESULT 1
CJ425530

LOCUS CJ425530 845 bp mRNA linear EST 21-JUN-2005

DEFINITION CJ425530 *Molgula tectiformis* unpublished cDNA library, larva
Molgula tectiformis cDNA clone mt1v024d01 3', mRNA sequence.

ACCESSION CJ425530

VERSION CJ425530.1 GI:68118069

KEYWORDS EST.

SOURCE *Molgula tectiformis*

ORGANISM *Molgula tectiformis*
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
Stolidobranchia; Molgulidae; *Molgula*.

REFERENCE 1 (bases 1 to 845)

AUTHORS Gyoja, F., Satou, Y. and Satoh, N.

TITLE Expressed genes in *Molgula tectiformis*

JOURNAL Unpublished (2005)

COMMENT Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan

SCORE Search Results Details for Application 10630536

Search Result us-10-630-536-3.rng.

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This page gives you Search Results detail for the Application 10630536 and Search Result us-10-630-536-3.rng. [start](#)

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OM nucleic - nucleic search, using sw model

Run on: July 1, 2006, 03:53:57 ; Search time 198.947 Seconds
(without alignments)
1156.508 Million cell updates/sec

Title: US-10-630-536-3

Perfect score: 33

Sequence: 1 catggaatcacacaaaaataatggcctcagatg 33

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : N_Geneseq_8:*
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14: geneseqn2005s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Query					Description
		Score	Match	Length	DB	ID	
	1	33	100.0	33	14	ADV04868	Adv04868 Yersinia
	2	33	100.0	102	14	ADV04869	Adv04869 Yersinia
c	3	33	100.0	100990	12	ADJ94407	Adj94407 Yersinia
	4	21.8	66.1	1722	10	ACF68430	Acf68430 Photorhab
	5	21.8	66.1	102644	10	ACF65378	Acf65378 Photorhab
	6	21.8	66.1	110000	10	ACF67367_11	Continuation (12 o
c	7	21.4	64.8	2081	12	ADP04087	Adp04087 Human col
	8	21	63.6	214019	10	ADL13809	Adl13809 Osteoarth
c	9	20.8	63.0	101169	12	ADQ97584	Adq97584 Mouse can
	10	20.6	62.4	161051	13	ABD32811	Abd32811 Human can
c	11	20.4	61.8	130263	6	ABK83573	Abk83573 Human cDN
c	12	20.2	61.2	1989	4	AAS03890	Aas03890 Human sec
	13	20.2	61.2	3093	12	ADP04510	Adp04510 Sea squir
c	14	20.2	61.2	52746	14	AEA61129	Aea61129 Human FLJ
c	15	20.2	61.2	74234	11	ACN44594	Acn44594 Human gen
	16	20.2	61.2	110000	11	ACN43998_3	Continuation (4 of
c	17	20	60.6	3638	4	ABL12764	Abl12764 Drosophil
	18	20	60.6	110000	14	AEE04876_6	Continuation (7 of
c	19	19.8	60.0	2669	12	ADO15889	Ado15889 4 synthes
c	20	19.8	60.0	29555	4	ABL18446	Abl18446 Drosophil
c	21	19.8	60.0	44748	11	ACN44064	Acn44064 Mouse gen
c	22	19.8	60.0	94330	11	ACN44662	Acn44662 Human gen
	23	19.8	60.0	116585	11	ACN43936	Acn43936 Mouse gen
c	24	19.8	60.0	209484	11	ACN44126	Acn44126 Human gen
c	25	19.6	59.4	313	13	ADU13837	Adu13837 Solid tum
c	26	19.6	59.4	3164	13	ADQ84812	Adq84812 Human tum
c	27	19.6	59.4	3164	13	ACN40700	Acn40700 Tumour-as
c	28	19.6	59.4	3188	6	ABL61777	Abl61777 Colon ade
c	29	19.6	59.4	3188	9	ACC85162	Acc85162 Human P13
c	30	19.6	59.4	3188	10	ADD29777	Add29777 Human tum
c	31	19.6	59.4	3190	2	AAZ11494	Aaz11494 Human pro
c	32	19.6	59.4	5173	4	ABL14096	Abl14096 Drosophil
c	33	19.4	58.8	852	2	AAX20460	Aax20460 Human sec
c	34	19.4	58.8	852	10	ADD90244	Add90244 Novel hum
c	35	19.4	58.8	852	10	ADG90063	Adg90063 Human cDN
c	36	19.4	58.8	852	14	ADY25403	Ady25403 Novel hum
c	37	19.4	58.8	1585	2	AAX97973	Aax97973 Human sec
c	38	19.4	58.8	1585	9	ADA11516	Ada11516 Human cDN
	39	19.4	58.8	2574	12	ADQ86023	Adq86023 Human tum
	40	19.4	58.8	2574	12	ADQ87487	Adq87487 Human tum
	41	19.4	58.8	2589	2	AAZ28760	Aaz28760 Human cyc
c	42	19.4	58.8	2775	11	ADM02633	Adm02633 Human cDN
c	43	19.4	58.8	2775	14	AEC85563	Aec85563 Human cDN
	44	19.4	58.8	3687	13	ADT05296	Adt05296 Haemophil
	45	19.4	58.8	3853	6	ABZ35020	Abz35020 Human gen
	46	19.4	58.8	3853	8	ACC50145	Acc50145 Breast ca
	47	19.4	58.8	3871	5	AAS87444	Aas87444 DNA encod
	48	19.4	58.8	4213	13	ADR07118	Adr07118 Full leng
	49	19.4	58.8	4863	14	AEB25798	Aeb25798 DNA encod
	50	19.4	58.8	4864	14	AEB25804	Aeb25804 DNA encod
	51	19.4	58.8	4864	14	AEB25802	Aeb25802 DNA encod
	52	19.4	58.8	4864	14	AEB25796	Aeb25796 DNA encod
	53	19.4	58.8	4864	14	AEB25800	Aeb25800 DNA encod
	54	19.4	58.8	4864	14	AEB25794	Aeb25794 DNA encod
	55	19.4	58.8	6147	8	ACC46453	Acc46453 Human dit
	56	19.4	58.8	9100	2	AAT28521	Aat28521 H. influe

57	19.4	58.8	9100	4	ABA76851	Aba76851 Haemophil
c 58	19.4	58.8	110000	2	AAT42063_04	Continuation (5 of
c 59	19.4	58.8	110000	6	ABQ74964_5	Continuation (6 of
c 60	19.4	58.8	117576	13	ADT05736	Adt05736 Haemophil
61	19.4	58.8	189013	8	ACF62741	Acf62741 Cancer ba
62	19.4	58.8	189013	8	ADB20856	Adb20856 MRP1 base
63	19.4	58.8	189013	10	ADB87945	Adb87945 Human UGT
64	19.4	58.8	189013	10	ADB96928	Adb96928 Human MDR
65	19.4	58.8	189013	10	ADB92119	Adb92119 Human MDR
66	19.2	58.2	653	6	ABQ59694	Abq59694 Human col
c 67	19.2	58.2	731	8	ABZ20574	Abz20574 Cancer as
c 68	19.2	58.2	778	4	AAK63403	Aak63403 Human imm
c 69	19.2	58.2	778	4	AAK84849	Aak84849 Human imm
c 70	19.2	58.2	778	4	AAK84850	Aak84850 Human imm
71	19.2	58.2	888	4	AAH01673	Aah01673 Microspor
c 72	19.2	58.2	1041	13	ADT05031	Adt05031 Haemophil
c 73	19.2	58.2	1437	13	ADO82662	Ado82662 Plant ful
c 74	19.2	58.2	1451	13	ADX49728	Adx49728 Plant ful
c 75	19.2	58.2	1528	13	ADX54310	Adx54310 Plant ful
76	19.2	58.2	2785	4	ABL08936	Abl08936 Drosophil
77	19.2	58.2	4362	4	ABL09880	Abl09880 Drosophil
78	19.2	58.2	4842	12	ADN72188	Adn72188 Thale cre
c 79	19.2	58.2	13236	12	ADQ21058	Adq21058 Human sof
c 80	19.2	58.2	53981	11	ACN44928	Acn44928 Mouse gen
81	19.2	58.2	78056	8	ABV99701	Abv99701 Bovine BS
82	19.2	58.2	78056	15	AEE20443	Aee20443 Bovine pr
c 83	19.2	58.2	170170	10	ADL13643	Adl13643 Osteoarth
84	19.2	58.2	191996	13	ADT05647	Adt05647 Haemophil
c 85	19.2	58.2	217409	11	ACN45150	Acn45150 Human gen
c 86	19	57.6	492	5	ABA14023	Abal4023 Human ner
87	19	57.6	2513	12	ADQ67417	Adq67417 Novel hum
c 88	19	57.6	32183	4	AAS35994	Aas35994 Human car
c 89	19	57.6	32183	10	ADE46688	Ade46688 Human car
c 90	19	57.6	32183	13	ADJ08106	Adj08106 Human car
91	19	57.6	32190	5	AAS29937	Aas29937 Human lun
92	19	57.6	32190	10	ADB33274	Adb33274 Human nov
93	19	57.6	32193	5	AAS29936	Aas29936 Human lun
94	19	57.6	32193	10	ADB33273	Adb33273 Human nov
95	19	57.6	51558	13	ACN37207	Acn37207 Human per
96	19	57.6	51935	4	AAK75883	Aak75883 Human imm
97	19	57.6	110000	6	ABA03041_25	Continuation (26 o
98	19	57.6	118951	8	ABT17385	Abt17385 Human IG
c 99	18.8	57.0	121	12	ADK92706	Adk92706 Polynucle
c 100	18.8	57.0	201	13	ADS39739	Ads39739 Human aut
101	18.8	57.0	245	2	AAT09778	Aat09778 Tomato ge
102	18.8	57.0	314	3	AAC28325	Aac28325 Human sec
103	18.8	57.0	363	5	ADI68108	Adi68108 Human ova
104	18.8	57.0	363	5	ADI74480	Adi74480 Human ova
105	18.8	57.0	374	5	AAF67183	Aaf67183 Novel hum
106	18.8	57.0	380	5	AAF67191	Aaf67191 Novel hum
107	18.8	57.0	380	11	ACN87001	Acn87001 Breast ca
108	18.8	57.0	396	4	AAL11455	Aal11455 Human bre
109	18.8	57.0	411	5	ADL39717	Adl39717 Human ova
110	18.8	57.0	416	9	ACH47499	Ach47499 Human inf
111	18.8	57.0	430	4	AAL20354	Aal20354 Human bre
c 112	18.8	57.0	454	2	AAX83400	Aax83400 Breast ca
c 113	18.8	57.0	454	2	AAV68935	Aav68935 DNA molec
c 114	18.8	57.0	454	3	AAC80923	Aac80923 Human bre
c 115	18.8	57.0	454	6	AAS99769	Aas99769 Breast tu
c 116	18.8	57.0	454	6	ABK46813	Abk46813 Human bre
c 117	18.8	57.0	454	8	ADA11290	Adal11290 Human bre

c 118	18.8	57.0	454	10	ADC15263	Adc15263 Human bre
119	18.8	57.0	541	11	ACN81656	Acn81656 Breast ca
120	18.8	57.0	567	13	ACN48276	Acn48276 Cotton pr
c 121	18.8	57.0	583	7	ADS72103	Ads72103 Human kid
c 122	18.8	57.0	583	7	ADW40957	Adw40957 cDNA elev
123	18.8	57.0	599	9	ACH27358	Ach27358 Human adu
124	18.8	57.0	615	6	ABK92240	Abk92240 Prostate
125	18.8	57.0	634	6	AAS99871	Aas99871 Breast tu
126	18.8	57.0	634	8	ADA11406	Ada11406 Human bre
127	18.8	57.0	634	10	ADC15379	Adc15379 Human bre
128	18.8	57.0	641	10	ABT21894	Abt21894 Breast ca
129	18.8	57.0	687	9	ADB83179	Adb83179 Human cDN
130	18.8	57.0	687	12	ADQ22655	Adq22655 Human sof
131	18.8	57.0	695	9	ADB82602	Adb82602 Human cDN
132	18.8	57.0	735	5	AAS76643	Aas76643 DNA encod
133	18.8	57.0	768	6	ABQ89662	Abq89662 Human pro
134	18.8	57.0	808	13	ADP55689	Adp55689 Human PRO
135	18.8	57.0	874	9	ADB83260	Adb83260 Human cDN
136	18.8	57.0	876	10	ADC15394	Adc15394 Human bre
137	18.8	57.0	876	10	ADC15393	Adc15393 Human bre
138	18.8	57.0	879	3	AAC81016	Aac81016 Human bre
139	18.8	57.0	879	4	AAH93826	Aah93826 Human pro
140	18.8	57.0	879	4	AAI94008	Aai94008 Human neu
141	18.8	57.0	879	4	AAS63919	Aas63919 Human pro
142	18.8	57.0	879	4	AAH85140	Aah85140 Human pro
143	18.8	57.0	879	5	ACA59727	Aca59727 Prostate
144	18.8	57.0	879	6	ABL95290	Abl95290 Human B30
145	18.8	57.0	879	6	AAS99862	Aas99862 Breast tu
146	18.8	57.0	879	8	ACC95454	Acc95454 Prostate
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148	18.8	57.0	879	10	ADC15366	Adc15366 Human bre
149	18.8	57.0	879	10	ADB13981	Adb13981 Human pro
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ALIGNMENTS

RESULT 1

ADV04868

ID ADV04868 standard; DNA; 33 BP.

XX

AC ADV04868;

XX

DT 24-FEB-2005 (first entry)

XX

DE Yersinia pestis amplicon #1 probe.

XX

KW Diagnosis; gene amplification; yersinia pestis infection; ss; probe.

XX

OS Yersinia pestis.

XX

PN WO2004106553-A2.

XX

PD 09-DEC-2004.

XX

PF 31-JUL-2003; 2003WO-US024135.

XX

PR -01-AUG-2002; 2002US-0400890P.

PR 29-JUL-2003; 2003US-00400890.

XX

SCORE Search Results Details for Application 10630536 and Search Result us-10-630-536-3.r

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This page gives you Search Results detail for the Application 10630536 and Search Result us-10-630-536-3.r.ni.

[start](#)

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OM nucleic - nucleic search, using sw model

Run on: July 1, 2006, 04:28:37 ; Search time 40.5 Seconds
(without alignments)
1524.607 Million cell updates/sec

Title: US-10-630-536-3

Perfect score: 33

Sequence: 1 catggaatcacacaaaaataatggcctcagatg 33

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	SUMMARIES			
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					Description

c	1	33	100.0	100990	3	US-09-409-800B-2	Sequence 2, Appli
c	2	20	60.6	390416	3	US-09-949-016-16923	Sequence 16923, A
c	3	19.8	60.0	601	3	US-09-949-016-33518	Sequence 33518, A
c	4	19.8	60.0	601	3	US-09-949-016-60370	Sequence 60370, A
	5	19.8	60.0	601	3	US-09-949-016-149247	Sequence 149247,
	6	19.8	60.0	1127	3	US-09-270-767-14416	Sequence 14416, A
	7	19.8	60.0	47347	3	US-09-949-016-14130	Sequence 14130, A
	8	19.8	60.0	49721	3	US-09-949-016-17538	Sequence 17538, A
c	9	19.8	60.0	128516	3	US-09-949-016-13501	Sequence 13501, A
c	10	19.8	60.0	133157	3	US-09-949-016-12541	Sequence 12541, A
c	11	19.8	60.0	187169	3	US-09-949-016-12776	Sequence 12776, A
c	12	19.8	60.0	191569	3	US-09-949-016-15940	Sequence 15940, A
	13	19.4	58.8	2589	2	US-08-482-728A-3	Sequence 3, Appli
	14	19.4	58.8	9100	2	US-08-743-637B-27	Sequence 27, Appli
	15	19.4	58.8	9100	3	US-08-526-840B-27	Sequence 27, Appli
c	16	19.4	58.8	117838	3	US-09-949-016-17595	Sequence 17595, A
c	17	19.4	58.8	786431	3	US-09-751-389-3	Sequence 3, Appli
c	18	19.4	58.8	1830121	3	US-09-557-884-1	Sequence 1, Appli
c	19	19.4	58.8	1830121	3	US-09-643-990A-1	Sequence 1, Appli
c	20	19.4	58.8	1830121	3	US-10-158-865-1	Sequence 1, Appli
	21	19.2	58.2	601	3	US-09-949-016-96617	Sequence 96617, A
	22	19.2	58.2	601	3	US-09-949-016-96618	Sequence 96618, A
	23	19.2	58.2	601	3	US-09-949-016-96883	Sequence 96883, A
	24	19.2	58.2	601	3	US-09-949-016-96884	Sequence 96884, A
	25	19.2	58.2	601	3	US-09-949-016-97149	Sequence 97149, A
	26	19.2	58.2	601	3	US-09-949-016-97150	Sequence 97150, A
	27	19.2	58.2	601	3	US-09-949-016-97415	Sequence 97415, A
	28	19.2	58.2	601	3	US-09-949-016-97416	Sequence 97416, A
	29	19.2	58.2	601	3	US-09-949-016-97681	Sequence 97681, A
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	38	19.2	58.2	601	3	US-09-949-016-98746	Sequence 98746, A
	39	19.2	58.2	601	3	US-09-949-016-99011	Sequence 99011, A
	40	19.2	58.2	601	3	US-09-949-016-99012	Sequence 99012, A
	41	19.2	58.2	601	3	US-09-949-016-99277	Sequence 99277, A
	42	19.2	58.2	601	3	US-09-949-016-99278	Sequence 99278, A
	43	19.2	58.2	601	3	US-09-949-016-99543	Sequence 99543, A
	44	19.2	58.2	601	3	US-09-949-016-99544	Sequence 99544, A
	45	19.2	58.2	601	3	US-09-949-016-99809	Sequence 99809, A
	46	19.2	58.2	601	3	US-09-949-016-99810	Sequence 99810, A
	47	19.2	58.2	601	3	US-09-949-016-100075	Sequence 100075,
	48	19.2	58.2	601	3	US-09-949-016-100076	Sequence 100076,
	49	19.2	58.2	601	3	US-09-949-016-100341	Sequence 100341,
	50	19.2	58.2	601	3	US-09-949-016-100342	Sequence 100342,
	51	19.2	58.2	601	3	US-09-949-016-100607	Sequence 100607,
	52	19.2	58.2	601	3	US-09-949-016-100608	Sequence 100608,
	53	19.2	58.2	601	3	US-09-949-016-100873	Sequence 100873,
	54	19.2	58.2	601	3	US-09-949-016-100874	Sequence 100874,
	55	19.2	58.2	601	3	US-09-949-016-100929	Sequence 100929,
	56	19.2	58.2	601	3	US-09-949-016-100930	Sequence 100930,
	57	19.2	58.2	601	3	US-09-949-016-101177	Sequence 101177,
	58	19.2	58.2	601	3	US-09-949-016-101178	Sequence 101178,
	59	19.2	58.2	601	3	US-09-949-016-101443	Sequence 101443,
	60	19.2	58.2	601	3	US-09-949-016-101444	Sequence 101444,

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OM nucleic - nucleic search, using sw model

Run on: July 1, 2006, 04:38:10 ; Search time 459.395 Seconds
(without alignments)
882.666 Million cell updates/sec

Title: US-10-630-536-3
Perfect score: 33
Sequence: 1 catggaatcacacaaaaataatggcctcagatg 33

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : Published_Applications_NA_Main:
1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*

2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*

3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*

5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*

6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*

7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*

9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*

10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*

11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*

12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*

13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*

14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*

15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*

16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	33	100.0	33	11	US-10-630-536-3	Sequence 3, Appli
2	33	100.0	102	11	US-10-630-536-4	Sequence 4, Appli
c 3	22.4	67.9	598	12	US-10-301-480-454944	Sequence 454944,
c 4	22.4	67.9	598	12	US-10-301-480-454945	Sequence 454945,
c 5	22.4	67.9	598	12	US-10-301-480-454946	Sequence 454946,
c 6	22.4	67.9	598	12	US-10-301-480-1068353	Sequence 1068353,
c 7	22.4	67.9	598	12	US-10-301-480-1068354	Sequence 1068354,
c 8	22.4	67.9	598	12	US-10-301-480-1068355	Sequence 1068355,
c 9	22.4	67.9	620	4	US-09-925-065A-386363	Sequence 386363,
c 10	22.4	67.9	620	4	US-09-925-065A-386364	Sequence 386364,
c 11	22.4	67.9	620	4	US-09-925-065A-386365	Sequence 386365,
c 12	22.4	67.9	620	5	US-09-925-065A-386363	Sequence 386363,
c 13	22.4	67.9	620	5	US-09-925-065A-386364	Sequence 386364,
c 14	22.4	67.9	620	5	US-09-925-065A-386365	Sequence 386365,
c 15	22	66.7	598	12	US-10-301-480-454943	Sequence 454943,
c 16	22	66.7	598	12	US-10-301-480-1068352	Sequence 1068352,
c 17	22	66.7	620	4	US-09-925-065A-386362	Sequence 386362,
c 18	22	66.7	620	5	US-09-925-065A-386362	Sequence 386362,
c 19	20.8	63.0	1672	10	US-10-750-185-35124	Sequence 35124, A
c 20	20.8	63.0	1672	10	US-10-750-623-35124	Sequence 35124, A
c 21	20.8	63.0	85506	7	US-10-085-117-220	Sequence 220, App
c 22	20.8	63.0	101169	11	US-10-330-773-561	Sequence 561, App
23	20.6	62.4	161051	9	US-10-417-375-170	Sequence 170, App
24	20.4	61.8	600	10	US-10-972-079-90890	Sequence 90890, A
25	20.4	61.8	600	10	US-10-972-079-90891	Sequence 90891, A
26	20.4	61.8	600	10	US-10-972-079-90892	Sequence 90892, A
27	20.4	61.8	600	10	US-10-972-079-90893	Sequence 90893, A
28	20.4	61.8	761	6	US-10-027-632-33780	Sequence 33780, A
29	20.4	61.8	761	6	US-10-027-632-33781	Sequence 33781, A
30	20.4	61.8	761	7	US-10-027-632-33780	Sequence 33780, A
31	20.4	61.8	761	7	US-10-027-632-33781	Sequence 33781, A
32	20.4	61.8	1663	4	US-09-925-065A-723444	Sequence 723444,
33	20.4	61.8	1663	5	US-09-925-065A-723444	Sequence 723444,
34	20.2	61.2	271	4	US-09-925-065A-524709	Sequence 524709,
35	20.2	61.2	271	4	US-09-925-065A-524710	Sequence 524710,
36	20.2	61.2	271	5	US-09-925-065A-524709	Sequence 524709,
37	20.2	61.2	271	5	US-09-925-065A-524710	Sequence 524710,
38	20.2	61.2	514	4	US-09-925-065A-260898	Sequence 260898,
39	20.2	61.2	514	5	US-09-925-065A-260898	Sequence 260898,
40	20.2	61.2	525	12	US-10-301-480-339238	Sequence 339238,
41	20.2	61.2	525	12	US-10-301-480-952647	Sequence 952647,
c 42	20.2	61.2	574	4	US-09-925-065A-269821	Sequence 269821,
c 43	20.2	61.2	574	5	US-09-925-065A-269821	Sequence 269821,
c 44	20.2	61.2	579	12	US-10-301-480-347363	Sequence 347363,
c 45	20.2	61.2	579	12	US-10-301-480-960772	Sequence 960772,
46	20.2	61.2	586	4	US-09-925-065A-608330	Sequence 608330,
47	20.2	61.2	586	4	US-09-925-065A-608331	Sequence 608331,
48	20.2	61.2	586	4	US-09-925-065A-608332	Sequence 608332,
49	20.2	61.2	586	4	US-09-925-065A-608333	Sequence 608333,
50	20.2	61.2	586	5	US-09-925-065A-608330	Sequence 608330,
51	20.2	61.2	586	5	US-09-925-065A-608331	Sequence 608331,

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OM nucleic - nucleic search, using sw model

Run on: July 1, 2006, 04:39:12 ; Search time 34.2632 Seconds
(without alignments)
1138.902 Million cell updates/sec

Title: US-10-630-536-3

Perfect score: 33

Sequence: 1 catggaaatcacacaaaaataatggcctcagatg 33

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 809770 seqs, 591248006 residues

Total number of hits satisfying chosen parameters: 1619540

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : Published_Applications_NA_New:
1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_NEW_PUB.seq:*

2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq:*

3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq:*

5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB.seq:*

6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*

7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:*

8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%
	Query

No.	Score	Match	Length	DB	ID	Description
c 1	20.8	63.0	1548	7	US-11-266-748A-180468	Sequence 180468,
c 2	20.8	63.0	1548	7	US-11-266-748A-240706	Sequence 240706,
c 3	20.4	61.8	130263	7	US-11-266-748A-58551	Sequence 58551, A
c 4	19.8	60.0	385	7	US-11-266-748A-252438	Sequence 252438,
c 5	19.8	60.0	385	7	US-11-266-748A-312955	Sequence 312955,
c 6	19.8	60.0	597	7	US-11-266-748A-267118	Sequence 267118,
c 7	19.8	60.0	597	7	US-11-266-748A-280557	Sequence 280557,
c 8	19.8	60.0	597	7	US-11-266-748A-327635	Sequence 327635,
c 9	19.8	60.0	421987	7	US-11-266-748A-28210	Sequence 28210, A
c 10	19.6	59.4	387	7	US-11-266-748A-178565	Sequence 178565,
c 11	19.6	59.4	415	7	US-11-266-748A-4042	Sequence 4042, Ap
c 12	19.6	59.4	879	7	US-11-266-748A-41287	Sequence 41287, A
c 13	19.6	59.4	1000	7	US-11-266-748A-116706	Sequence 116706,
c 14	19.6	59.4	1000	7	US-11-266-748A-158870	Sequence 158870,
c 15	19.6	59.4	1000	7	US-11-266-748A-221937	Sequence 221937,
c 16	19.6	59.4	1000	7	US-11-266-748A-287513	Sequence 287513,
c 17	19.6	59.4	1000	7	US-11-266-748A-338942	Sequence 338942,
c 18	19.6	59.4	1000	7	US-11-266-748A-398227	Sequence 398227,
c 19	19.6	59.4	1000	7	US-11-266-748A-469273	Sequence 469273,
c 20	19.6	59.4	1118	7	US-11-266-748A-69120	Sequence 69120, A
c 21	19.6	59.4	1118	7	US-11-266-748A-121931	Sequence 121931,
c 22	19.6	59.4	1478	7	US-11-266-748A-251523	Sequence 251523,
c 23	19.6	59.4	1478	7	US-11-266-748A-275484	Sequence 275484,
c 24	19.6	59.4	1478	7	US-11-266-748A-312040	Sequence 312040,
c 25	19.6	59.4	3158	7	US-11-266-748A-31538	Sequence 31538, A
c 26	19.6	59.4	3204	7	US-11-266-748A-31537	Sequence 31537, A
c 27	19.6	59.4	3241	7	US-11-266-748A-29773	Sequence 29773, A
c 28	19.4	58.8	555	7	US-11-266-748A-168573	Sequence 168573,
c 29	19.4	58.8	893	7	US-11-266-748A-182628	Sequence 182628,
c 30	19.4	58.8	976	7	US-11-266-748A-356698	Sequence 356698,
c 31	19.4	58.8	976	7	US-11-266-748A-440077	Sequence 440077,
c 32	19.4	58.8	1618	7	US-11-266-748A-93308	Sequence 93308, A
c 33	19.4	58.8	1618	7	US-11-266-748A-146119	Sequence 146119,
c 34	19.4	58.8	2081	7	US-11-266-748A-186932	Sequence 186932,
c 35	19.4	58.8	2081	7	US-11-266-748A-241617	Sequence 241617,
c 36	19.4	58.8	2775	7	US-11-293-697-1318	Sequence 1318, Ap
c 37	19.4	58.8	3853	7	US-11-302-033-1	Sequence 1, Appli
c 38	19.4	58.8	3853	7	US-11-266-748A-28964	Sequence 28964, A
c 39	19.2	58.2	932	6	US-10-953-349-18568	Sequence 18568, A
c 40	19.2	58.2	1449	6	US-10-953-349-13505	Sequence 13505, A
c 41	19.2	58.2	1480	6	US-10-953-349-21936	Sequence 21936, A
c 42	19.2	58.2	2089	6	US-10-449-902-10155	Sequence 10155, A
c 43	19.2	58.2	4006	6	US-10-449-902-28263	Sequence 28263, A
c 44	19.2	58.2	200033	7	US-11-266-748A-23936	Sequence 23936, A
c 45	19	57.6	417	7	US-11-266-748A-360929	Sequence 360929,
c 46	19	57.6	417	7	US-11-266-748A-444308	Sequence 444308,
c 47	19	57.6	131546	7	US-11-266-748A-60109	Sequence 60109, A
c 48	18.8	57.0	387	7	US-11-266-748A-36485	Sequence 36485, A
c 49	18.8	57.0	653	7	US-11-266-748A-49300	Sequence 49300, A
c 50	18.8	57.0	780	7	US-11-217-529-77764	Sequence 77764, A
c 51	18.8	57.0	822	7	US-11-266-748A-55221	Sequence 55221, A
c 52	18.8	57.0	864	7	US-11-266-748A-1000	Sequence 1000, Ap
c 53	18.8	57.0	864	7	US-11-266-748A-62726	Sequence 62726, A
c 54	18.8	57.0	864	7	US-11-266-748A-65558	Sequence 65558, A
c 55	18.8	57.0	875	7	US-11-266-748A-165742	Sequence 165742,
c 56	18.8	57.0	1006	6	US-10-525-126-108	Sequence 108, App
c 57	18.8	57.0	1079	7	US-11-266-748A-186067	Sequence 186067,
c 58	18.8	57.0	1079	7	US-11-266-748A-193429	Sequence 193429,
c 59	18.8	57.0	1079	7	US-11-266-748A-241205	Sequence 241205,

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OM nucleic - nucleic search, using sw model

Run on: July 1, 2006, 04:17:07 ; Search time 1197.08 Seconds
(without alignments)
1541.534 Million cell updates/sec

Title: US-10-630-536-3
Perfect score: 33
Sequence: 1 catggaatcacacaaaaataatggcctcagatg 33

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : EST:
1: gb_est1:
2: gb_est3:
3: gb_est4:
4: gb_est5:
5: gb_est6:
6: gb_htc:
7: gb_est2:
8: gb_est7:
9: gb_est8:
10: gb_est9:
11: gb_gss1:
12: gb_gss2:
13: gb_gss3:
14: gb_gss4:

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Score	Query				Description
		Match	Length	DB	ID	
	1	23	69.7	644	14	CR029088
c	2	23	69.7	741	14	CR210450
	3	22.6	68.5	1076	12	CC232438
c	4	22.4	67.9	610	3	BU479093
	5	22.4	67.9	755	14	AG495577
	6	22	66.7	584	3	BP529535
	7	21.8	66.1	323	11	BZ212891
	8	21.8	66.1	535	13	CZ204066
	9	21.8	66.1	699	14	CT093861
	10	21.8	66.1	719	14	CT152488
	11	21.8	66.1	740	14	AG162543
	12	21.8	66.1	915	14	DU517106
	13	21.6	65.5	595	11	AQ880712
c	14	21.6	65.5	658	8	CN949960
c	15	21.6	65.5	904	12	CG813163
c	16	21.4	64.8	542	13	DU284843
c	17	21.4	64.8	609	14	CT150101
c	18	21.4	64.8	663	4	BX507342
	19	21.4	64.8	1101	14	CNS00FW1
	20	21.2	64.2	547	1	AA472123
	21	21.2	64.2	547	10	DT902166
	22	21.2	64.2	547	10	DT908521
	23	21.2	64.2	617	2	BG077133
c	24	21.2	64.2	696	14	DU529868
	25	21.2	64.2	872	4	CB203027
	26	21.2	64.2	3409	6	AK034075
	27	21	63.6	493	7	BF041073
c	28	21	63.6	564	14	CR205643
	29	21	63.6	663	4	BY746719
c	30	21	63.6	730	14	AG075415
c	31	21	63.6	765	12	BZ774479
	32	21	63.6	786	9	DN043441
c	33	21	63.6	936	14	CNS03EE0
c	34	21	63.6	1006	13	CW958942
	35	20.8	63.0	251	5	CD933887
	36	20.8	63.0	325	11	AQ361021
c	37	20.8	63.0	421	2	BF987726
	38	20.8	63.0	456	12	CC888070
	39	20.8	63.0	459	4	CB075617
	40	20.8	63.0	473	7	BE165959
c	41	20.8	63.0	473	11	AQ407551
	42	20.8	63.0	475	8	CV030602
c	43	20.8	63.0	480	5	CJ139390
	44	20.8	63.0	493	11	AZ289232
c	45	20.8	63.0	520	4	BW552416
c	46	20.8	63.0	532	2	BI705970
c	47	20.8	63.0	532	4	BW568160
	48	20.8	63.0	537	9	DB214916
	49	20.8	63.0	538	11	BH737892
c	50	20.8	63.0	547	9	DA380460
c	51	20.8	63.0	556	4	BW584091
c	52	20.8	63.0	560	4	BW554235
c	53	20.8	63.0	569	12	CE685767

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OM nucleic - nucleic search, using sw model

Run on: July 1, 2006, 03:55:42 ; Search time 1520 Seconds
(without alignments)
4291.222 Million cell updates/sec

Title: US-10-630-536-4

Perfect score: 102

Sequence: 1 atttccccaccaatcaacgt.....tggacataaacatgaacatgg 102

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

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10: gb_vi:
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12: gb_htg:
13: gb_in:
14: gb_om:
15: gb_ba:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c 4	102	100.0	100984	15	AF053947		AF053947 Yersinia
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c 11	34.4	33.7	266486	12	AC173090		AC173090 Bos tauru
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c 13	34	33.3	205171	12	CR354612		CR354612 Danio rer
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15	34	33.3	229567	12	CR394539		CR394539 Danio rer
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	96	30	29.4	652	7	BV432809	BV432809 S237P6430
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c 116	29.6	29.0	36307	12	AY714849	AY714849 Unculture
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c 147	29.4	28.8	110000	13	CP000224_1	Continuation (2 of
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ALIGNMENTS

RESULT 1
 CS001823

LOCUS CS001823 102 bp DNA linear PAT 01-FEB-2005

DEFINITION Sequence 4 from Patent WO2004106553.

ACCESSION CS001823

VERSION CS001823.1 GI:58424078

KEYWORDS .

SOURCE Yersinia pestis

ORGANISM Yersinia pestis
 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 Enterobacteriaceae; Yersinia.

REFERENCE 1

AUTHORS McCready, P.M., Radnedge, L., Andersen, G.L., Ott, L.L., Slezak, T.R.,
 Kuczmarski, T.A. and Motin, V.L.

TITLE Nucleotide sequences specific to Yersinia pestis and methods for
 the detection of Yersinia pestis

JOURNAL Patent: WO 2004106553-A 4 09-DEC-2004;
 The Regents of The University of California (US)

FEATURES Location/Qualifiers

SCORE Search Results Details for Application 10

10-630-536-1.rge

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OM nucleic - nucleic search, using sw model

Run on: July 1, 2006, 03:55:42 ; Search time 417.254 Seconds
 (without alignments)
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Title: US-10-630-536-1
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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 150 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	90	19	67.9	589	13	AF435115	AF435115 Eriocheir
	91	19	67.9	589	13	AF435116	AF435116 Eriocheir
	92	19	67.9	589	13	AF435117	AF435117 Eriocheir
	93	19	67.9	589	13	AF435118	AF435118 Eriocheir
	94	19	67.9	589	13	AF435119	AF435119 Eriocheir
	95	19	67.9	600	13	AF153922	AF153922 Euphydrya
	96	19	67.9	600	13	AF153935	AF153935 Chlosyne
	97	19	67.9	606	13	AY271850	AY271850 Paramphit
	98	19	67.9	615	13	AF000031	AF000031 Brachiote
	99	19	67.9	617	13	AF549680	AF549680 Aethalura
100	19	67.9	618	13	DQ292224	DQ292224 Corticea	
101	19	67.9	630	13	AY271851	AY271851 Paramphit	
102	19	67.9	632	13	AY271846	AY271846 Paramphit	
103	19	67.9	632	13	AY271847	AY271847 Paramphit	
104	19	67.9	632	13	AY271848	AY271848 Paramphit	
105	19	67.9	633	13	DQ293588	DQ293588 Telemiade	
106	19	67.9	647	13	AY601081	AY601081 Euphausia	
107	19	67.9	651	13	AY640082	AY640082 Eriocheir	
108	19	67.9	651	13	AY640083	AY640083 Eriocheir	
109	19	67.9	651	13	AY640084	AY640084 Eriocheir	
110	19	67.9	651	13	AY640085	AY640085 Eriocheir	
111	19	67.9	651	13	AY640086	AY640086 Eriocheir	
112	19	67.9	651	13	AY640087	AY640087 Eriocheir	
113	19	67.9	651	13	AY640095	AY640095 Eriocheir	
114	19	67.9	651	13	AY640096	AY640096 Eriocheir	
115	19	67.9	651	13	AY640097	AY640097 Eriocheir	
116	19	67.9	651	13	AY640098	AY640098 Eriocheir	
117	19	67.9	651	13	AY640099	AY640099 Eriocheir	

SCORE Search Results Details for Application 10630536

Search Result us-10-630-536-4.rng.

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This page gives you Search Results detail for the Application 10630536 and Search Result us-10-630-536-4.rng.
start

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: July 1, 2006, 03:53:57 ; Search time 614.928 Seconds
 (without alignments)
 1156.508 Million cell updates/sec

Title: US-10-630-536-4

Perfect score: 102

Sequence: 1 atttcccaccaatcaacgt.....tggacataaacatgaacatgg 102

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 150 summaries

Database : N_Geneseq_8:*
 1: geneseqn1980s:*
 2: geneseqn1990s:*
 3: geneseqn2000s:*
 4: geneseqn2001as:*
 5: geneseqn2001bs:*
 6: geneseqn2002as:*
 7: geneseqn2002bs:*
 8: geneseqn2003as:*
 9: geneseqn2003bs:*
 10: geneseqn2003cs:*
 11: geneseqn2003ds:*
 12: geneseqn2004as:*
 13: geneseqn2004bs:*
 14: geneseqn2005s:*
 15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Query					Description
		Score	Match	Length	DB	ID	
	1	102	100.0	102	14	ADV04869	Adv04869 Yersinia
c	2	102	100.0	100990	12	ADJ94407	Adj94407 Yersinia
	3	52.4	51.4	1722	10	ACF68430	Acf68430 Photorhab
	4	52.4	51.4	102644	10	ACF65378	Acf65378 Photorhab
	5	52.4	51.4	110000	10	ACF67367_11	Continuation (12 o
	6	33	32.4	33	14	ADV04868	Adv04868 Yersinia
	7	31.8	31.2	286	10	ABX88861	Abx88861 Corn ear-
	8	31.2	30.6	1428	13	ADX09957	Adx09957 Plant ful
	9	30.2	29.6	1488	6	ABN91973	Abn91973 Staphyloc
	10	30.2	29.6	1488	13	ADS00787	Ads00787 Staphyloc
	11	29	28.4	1670	13	ADX14182	Adx14182 Plant ful
	12	29	28.4	1676	13	ADX28565	Adx28565 Plant ful
	13	29	28.4	1678	13	ADX28109	Adx28109 Plant ful
c	14	29	28.4	110000	2	AAZ01425_00	Aaz01425 Complete
c	15	28.6	28.0	9062	2	AAV74396	Aav74396 Staphyloc
	16	28.6	28.0	43009	11	ACN44902	Acn44902 Human gen
c	17	28.6	28.0	338702	11	ACN44042	Acn44042 Human gen
	18	28.4	27.8	1183	2	AAV74787	Aav74787 Staphyloc
	19	28.4	27.8	1482	6	ABA51633	Aba51633 Staphyloc
	20	28.4	27.8	1482	10	ADC21335	Adc21335 Staphyloc
	21	28.4	27.8	1482	10	ADC25021	Adc25021 DNA encod
	22	28.4	27.8	1482	10	ADD52523	Add52523 Staphyloc
	23	28.4	27.8	1509	6	ABA51669	Aba51669 Staphyloc
	24	28.4	27.8	1509	10	ADC21401	Adc21401 Staphyloc
	25	28.4	27.8	1509	10	ADC25087	Adc25087 DNA encod
	26	28.4	27.8	1509	10	ADD52589	Add52589 Staphyloc
	27	28.4	27.8	1530	8	ACF73154	Acf73154 Staphyloc
c	28	28.4	27.8	1598	13	ADT14893	Adt14893 Plant cDN
	29	28.2	27.6	3883	13	ADR84624	Adr84624 Aspergill
	30	28.2	27.6	68255	11	ACN44362	Acn44362 Human gen
	31	28.2	27.6	110000	12	ADO79173_3	Continuation (4 of
c	32	28	27.5	28	14	ADV04867	Adv04867 Yersinia
	33	28	27.5	28	14	ADV04866	Adv04866 Yersinia
	34	28	27.5	721	13	ADX27687	Adx27687 Plant ful
	35	28	27.5	741	4	AAK82469	Aak82469 Human imm
c	36	28	27.5	1153	4	AAS23216	Aas23216 DNA encod
	37	28	27.5	3310	4	AAH54779	Aah54779 S. epider
	38	28	27.5	22970	10	ADK70082	Adk70082 Mutant hu
	39	28	27.5	22970	10	ADK70081	Adk70081 Wild type
c	40	28	27.5	59359	11	ACN44220	Acn44220 Mouse gen
	41	27.8	27.3	433	14	AEB27932	Aeb27932 Nematode
c	42	27.6	27.1	351	11	ACL29408	Acl29408 Rice abio
	43	27.6	27.1	1368	13	ADS47046	Ads47046 Bacterial
	44	27.6	27.1	1704	4	AAH84610	Aah84610 E. coli g
	45	27.6	27.1	1704	8	ACA18618	Aca18618 Prokaryot
	46	27.6	27.1	4740	13	ADS47257	Ads47257 Bacterial
c	47	27.6	27.1	5487	6	ABL33599	Ab133599 Human imm
c	48	27.4	26.9	121	12	ADK92706	Adk92706 Polynucle
	49	27.4	26.9	3548	13	ADX61552	Adx61552 Plant ful
c	50	27.4	26.9	9816	10	ACF71805	Acf71805 Photorhab
c	51	27.4	26.9	110000	10	ACF67367_50	Continuation (51 o
c	52	27.4	26.9	110000	10	ACF65387_1	Continuation (2 of
	53	27.4	26.9	110000	13	ABD32804_3	Continuation (4 of
	54	27.2	26.7	1101	12	ADP98577	Adp98577 C. albica
c	55	27.2	26.7	1803	6	AAS62426	Aas62426 cDNA sequ
	56	27.2	26.7	2677	4	ABL21388	Ab121388 Drosophil

SCORE Search Results Details for Application 10630536 and Search Result us-10-630-536-4.

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OM nucleic - nucleic search, using sw model

Run on: July 1, 2006, 04:28:37 ; Search time 125.182 Seconds
(without alignments)
1524.607 Million cell updates/sec

Title: US-10-630-536-4

Perfect score: 102

Sequence: 1 atttcccaccaatcaacatgat.....tggacataacatgaacatgg 102

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : Issued_Patents_NA:
1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*

2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*

3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*

4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*

5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*

6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*

7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*

8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*

9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*

10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query				
No.	Score	Match	Length	DB	ID
					Description

c	1	102	100.0	100990	3	US-09-409-800B-2	Sequence 2, Appli
	2	31.8	31.2	286	3	US-09-313-294A-7321	Sequence 7321, Ap
	3	30.2	29.6	1488	3	US-09-134-001C-1436	Sequence 1436, Ap
c	4	29.6	29.0	72504	3	US-09-949-016-14855	Sequence 14855, A
c	5	28.8	28.2	601	3	US-09-949-016-84207	Sequence 84207, A
c	6	28.6	28.0	9062	3	US-08-956-171E-85	Sequence 85, Appl
c	7	28.6	28.0	9062	3	US-08-781-986A-85	Sequence 85, Appl
	8	28.6	28.0	15817	3	US-09-949-016-16496	Sequence 16496, A
c	9	28.6	28.0	251672	3	US-09-949-016-17296	Sequence 17296, A
c	10	28.6	28.0	251682	3	US-09-949-016-11973	Sequence 11973, A
	11	28.4	27.8	1183	3	US-08-956-171E-476	Sequence 476, App
	12	28.4	27.8	1183	3	US-08-781-986A-476	Sequence 476, App
	13	28.4	27.8	1482	3	US-09-828-523A-21	Sequence 21, Appl
	14	28.4	27.8	1509	3	US-09-828-523A-89	Sequence 89, Appl
	15	28	27.5	3310	3	US-09-710-279-4143	Sequence 4143, Ap
c	16	28	27.5	25973	3	US-09-949-016-14140	Sequence 14140, A
	17	27.8	27.3	433	3	US-09-437-450A-38	Sequence 38, Appl
c	18	27.6	27.1	601	3	US-09-949-016-84206	Sequence 84206, A
	19	27.6	27.1	1368	3	US-09-614-221A-284	Sequence 284, App
	20	27.6	27.1	1704	3	US-09-711-164-238	Sequence 238, App
	21	27.6	27.1	4740	3	US-09-487-558B-367	Sequence 367, App
	22	27.6	27.1	117391	3	US-09-949-016-13945	Sequence 13945, A
c	23	27.6	27.1	455726	3	US-09-949-016-14157	Sequence 14157, A
c	24	27.6	27.1	481115	3	US-09-949-016-11940	Sequence 11940, A
c	25	27.2	26.7	601	3	US-09-949-002-3629	Sequence 3629, Ap
c	26	27.2	26.7	601	3	US-09-949-002-3630	Sequence 3630, Ap
c	27	27.2	26.7	601	3	US-09-949-002-5474	Sequence 5474, Ap
c	28	27.2	26.7	601	3	US-09-949-002-5475	Sequence 5475, Ap
	29	27.2	26.7	1116	3	US-09-248-796A-3645	Sequence 3645, Ap
	30	27.2	26.7	10190	3	US-10-232-858-105	Sequence 105, App
	31	27.2	26.7	10190	3	US-09-338-063A-105	Sequence 105, App
c	32	27.2	26.7	59158	3	US-09-949-002-728	Sequence 728, App
c	33	27.2	26.7	64994	3	US-09-949-002-688	Sequence 688, App
c	34	27.2	26.7	75929	3	US-09-949-016-15543	Sequence 15543, A
c	35	27.2	26.7	75929	3	US-09-949-016-15544	Sequence 15544, A
c	36	27	26.5	113876	3	US-09-949-016-14828	Sequence 14828, A
c	37	27	26.5	113876	3	US-09-949-016-14829	Sequence 14829, A
c	38	27	26.5	115508	3	US-09-949-016-11800	Sequence 11800, A
c	39	27	26.5	115508	3	US-09-949-016-14826	Sequence 14826, A
c	40	27	26.5	115508	3	US-09-949-016-14827	Sequence 14827, A
	41	26.8	26.3	66109	4	US-09-880-107-3768	Sequence 3768, Ap
	42	26.8	26.3	198285	4	US-09-880-107-3814	Sequence 3814, Ap
	43	26.8	26.3	199471	3	US-09-949-016-14083	Sequence 14083, A
c	44	26.8	26.3	1830121	3	US-09-557-884-1	Sequence 1, Appli
c	45	26.8	26.3	1830121	3	US-09-643-990A-1	Sequence 1, Appli
c	46	26.8	26.3	1830121	3	US-10-158-865-1	Sequence 1, Appli
	47	26.6	26.1	3015	3	US-09-134-000C-2014	Sequence 2014, Ap
	48	26.4	25.9	528	5	US-09-974-300-6115	Sequence 6115, Ap
	49	26.4	25.9	582	5	US-09-974-300-6100	Sequence 6100, Ap
c	50	26.4	25.9	1501	3	US-09-774-528-231	Sequence 231, App
c	51	26.4	25.9	1501	3	US-10-120-988-231	Sequence 231, App
	52	26.4	25.9	1602	3	US-09-134-001C-1216	Sequence 1216, Ap
c	53	26.4	25.9	32392	3	US-09-662-254B-27	Sequence 27, Appl
	54	26.4	25.9	95750	3	US-09-949-016-11926	Sequence 11926, A
	55	26.2	25.7	1644	3	US-09-248-796A-2122	Sequence 2122, Ap
	56	26	25.5	601	3	US-09-949-016-38426	Sequence 38426, A
	57	26	25.5	601	3	US-09-949-016-176178	Sequence 176178,
	58	26	25.5	601	3	US-09-949-016-176231	Sequence 176231,
	59	26	25.5	601	3	US-09-949-016-176269	Sequence 176269,
	60	26	25.5	601	3	US-09-949-016-176307	Sequence 176307,

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OM nucleic - nucleic search, using sw model

Run on: July 1, 2006, 04:38:10 ; Search time 1419.95 Seconds
(without alignments)
882.666 Million cell updates/sec

Title: US-10-630-536-4
Perfect score: 102
Sequence: 1 atttcccaccaatcaacgat.....tggacataacatgaacatgg 102

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : Published_Applications_NA_Main:
1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*

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4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*

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6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*

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10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*

11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*

12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*

13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*

14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*

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16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	102	100.0	102	11	US-10-630-536-4	Sequence 4, Appli
2	33	32.4	33	11	US-10-630-536-3	Sequence 3, Appli
3	31.8	31.2	550	4	US-09-925-065A-116209	Sequence 116209,
4	31.8	31.2	550	5	US-09-925-065A-116209	Sequence 116209,
5	31.8	31.2	555	12	US-10-301-480-215091	Sequence 215091,
6	31.8	31.2	555	12	US-10-301-480-828500	Sequence 828500,
c 7	31.4	30.8	617	4	US-09-925-065A-482222	Sequence 482222,
c 8	31.4	30.8	617	4	US-09-925-065A-482223	Sequence 482223,
c 9	31.4	30.8	617	4	US-09-925-065A-482224	Sequence 482224,
c 10	31.4	30.8	617	5	US-09-925-065A-482222	Sequence 482222,
c 11	31.4	30.8	617	5	US-09-925-065A-482223	Sequence 482223,
c 12	31.4	30.8	617	5	US-09-925-065A-482224	Sequence 482224,
13	31.4	30.8	618	4	US-09-925-065A-486061	Sequence 486061,
14	31.4	30.8	618	5	US-09-925-065A-486061	Sequence 486061,
15	31.2	30.6	1428	8	US-10-425-114-4532	Sequence 4532, Ap
16	31	30.4	471	8	US-10-242-535A-44169	Sequence 44169, A
17	31	30.4	471	8	US-10-085-783A-44169	Sequence 44169, A
18	30.6	30.0	541	6	US-10-027-632-42175	Sequence 42175, A
19	30.6	30.0	541	7	US-10-027-632-42175	Sequence 42175, A
20	30.2	29.6	1488	8	US-10-724-972A-82	Sequence 82, Appl
21	29.6	29.0	2162	9	US-10-425-115-55632	Sequence 55632, A
c 22	29	28.4	777	4	US-09-925-065A-932706	Sequence 932706,
c 23	29	28.4	777	5	US-09-925-065A-932706	Sequence 932706,
24	29	28.4	1670	8	US-10-425-114-8757	Sequence 8757, Ap
25	29	28.4	1676	8	US-10-425-114-11385	Sequence 11385, A
26	29	28.4	1678	8	US-10-425-114-10929	Sequence 10929, A
27	29	28.4	2991	8	US-10-424-599-120243	Sequence 120243,
c 28	28.8	28.2	201	9	US-10-719-993-13830	Sequence 13830, A
29	28.8	28.2	520	6	US-10-027-632-282317	Sequence 282317,
30	28.8	28.2	520	7	US-10-027-632-282317	Sequence 282317,
31	28.6	28.0	192	9	US-10-674-124A-1114	Sequence 1114, Ap
32	28.6	28.0	579	6	US-10-027-632-34442	Sequence 34442, A
33	28.6	28.0	579	7	US-10-027-632-34442	Sequence 34442, A
c 34	28.6	28.0	9062	2	US-08-781-986A-85	Sequence 85, Appl
c 35	28.6	28.0	9062	8	US-10-329-624-85	Sequence 85, Appl
36	28.6	28.0	43009	6	US-10-087-192-1582	Sequence 1582, Ap
37	28.6	28.0	184868	15	US-11-121-086-88	Sequence 88, Appl
c 38	28.6	28.0	338702	6	US-10-087-192-292	Sequence 292, App
39	28.4	27.8	649	12	US-10-301-480-387907	Sequence 387907,
40	28.4	27.8	649	12	US-10-301-480-1001316	Sequence 1001316,
41	28.4	27.8	1183	2	US-08-781-986A-476	Sequence 476, App
42	28.4	27.8	1183	8	US-10-329-624-476	Sequence 476, App
43	28.4	27.8	1482	3	US-09-828-523A-21	Sequence 21, Appl
44	28.4	27.8	1482	3	US-09-966-521-17	Sequence 17, Appl
45	28.4	27.8	1482	7	US-10-429-094-17	Sequence 17, Appl
46	28.4	27.8	1509	3	US-09-828-523A-89	Sequence 89, Appl
47	28.4	27.8	1509	3	US-09-966-521-83	Sequence 83, Appl
48	28.4	27.8	1509	7	US-10-429-094-83	Sequence 83, Appl
c 49	28.4	27.8	1598	9	US-10-739-930-219	Sequence 219, App
c 50	28.4	27.8	493999	9	US-10-719-993-6787	Sequence 6787, Ap
51	28.4	27.8	1223197	6	US-10-027-632-179264	Sequence 179264,
52	28.4	27.8	1223197	7	US-10-027-632-179264	Sequence 179264,

SCORE Search Results Details for Application 10630536 and Search Result us-10-630-536-4.rnpbn.

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: July 1, 2006, 04:39:12 ; Search time 105.904 Seconds
(without alignments)
1138.902 Million cell updates/sec

Title: US-10-630-536-4

Perfect score: 102

Sequence: 1 atttcccaccaatcaacgt.....tggacataaacatgaacatgg 102

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 809770 seqs, 591248006 residues

Total number of hits satisfying chosen parameters: 1619540

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : Published_Applications_NA_New:
1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_NEW_PUB.seq:*

2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq:*

3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq:*

5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB.seq:*

6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*

7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:*

8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query

No.	Score	Match Length	DB	ID	Description
c 1	29.4	28.8	1909	6 US-10-953-349-10555	Sequence 10555, A
2	28.4	27.8	1530	6 US-10-471-571A-1667	Sequence 1667, Ap
3	27.6	27.1	2538	7 US-11-217-529-81150	Sequence 81150, A
c 4	27.4	26.9	808	7 US-11-266-748A-366887	Sequence 366887,
c 5	27.4	26.9	808	7 US-11-266-748A-388674	Sequence 388674,
6	27.4	26.9	808	7 US-11-266-748A-450266	Sequence 450266,
c 7	27.4	26.9	1184	7 US-11-266-748A-302007	Sequence 302007,
8	27.2	26.7	156655	7 US-11-266-748A-24308	Sequence 24308, A
9	26.8	26.3	2426	7 US-11-266-748A-188428	Sequence 188428,
c 10	26.8	26.3	2426	7 US-11-266-748A-242364	Sequence 242364,
11	26.8	26.3	66109	7 US-11-266-748A-32175	Sequence 32175, A
12	26.8	26.3	198285	7 US-11-266-748A-59857	Sequence 59857, A
13	26.6	26.1	2432	6 US-10-449-902-9730	Sequence 9730, Ap
c 14	26.6	26.1	160820	7 US-11-266-748A-22501	Sequence 22501, A
15	26.4	25.9	1000	7 US-11-266-748A-198483	Sequence 198483,
16	26.4	25.9	684973	7 US-11-266-748A-32013	Sequence 32013, A
c 17	26.2	25.7	1071650	7 US-11-266-748A-22664	Sequence 22664, A
18	26	25.5	1131	7 US-11-217-529-82398	Sequence 82398, A
19	26	25.5	2552	7 US-11-297-315-11	Sequence 11, Appl
20	26	25.5	2552	7 US-11-297-315-12	Sequence 12, Appl
c 21	26	25.5	128978	7 US-11-266-748A-61436	Sequence 61436, A
c 22	25.8	25.3	554	6 US-10-488-619-125	Sequence 125, App
23	25.8	25.3	1000	7 US-11-266-748A-115244	Sequence 115244,
c 24	25.8	25.3	1000	7 US-11-266-748A-157408	Sequence 157408,
c 25	25.8	25.3	1000	7 US-11-266-748A-202572	Sequence 202572,
26	25.8	25.3	1000	7 US-11-266-748A-392415	Sequence 392415,
27	25.8	25.3	1000	7 US-11-266-748A-393951	Sequence 393951,
c 28	25.8	25.3	1000	7 US-11-266-748A-464997	Sequence 464997,
c 29	25.8	25.3	1000	7 US-11-266-748A-483133	Sequence 483133,
30	25.8	25.3	1841	7 US-11-266-748A-20889	Sequence 20889, A
31	25.8	25.3	1854	7 US-11-266-748A-186789	Sequence 186789,
32	25.8	25.3	2237	6 US-10-449-902-27089	Sequence 27089, A
33	25.6	25.1	1000	7 US-11-266-748A-196364	Sequence 196364,
34	25.6	25.1	1253	6 US-10-449-902-1062	Sequence 1062, Ap
35	25.6	25.1	1512	6 US-10-449-902-22374	Sequence 22374, A
36	25.6	25.1	4611	7 US-11-217-529-191207	Sequence 191207,
c 37	25.4	24.9	1453	7 US-11-216-545-1367	Sequence 1367, Ap
38	25.4	24.9	1237661	7 US-11-266-748A-29041	Sequence 29041, A
39	25.2	24.7	502	7 US-11-266-748A-40402	Sequence 40402, A
c 40	25.2	24.7	572	7 US-11-266-748A-52577	Sequence 52577, A
41	25.2	24.7	597	7 US-11-266-748A-85668	Sequence 85668, A
c 42	25.2	24.7	597	7 US-11-266-748A-138479	Sequence 138479,
c 43	25.2	24.7	814	7 US-11-266-748A-44067	Sequence 44067, A
c 44	25.2	24.7	815	7 US-11-266-748A-177083	Sequence 177083,
c 45	25.2	24.7	874	7 US-11-266-748A-181798	Sequence 181798,
46	25.2	24.7	874	7 US-11-266-748A-242312	Sequence 242312,
c 47	25.2	24.7	918	7 US-11-266-748A-88079	Sequence 88079, A
48	25.2	24.7	918	7 US-11-266-748A-140890	Sequence 140890,
c 49	25.2	24.7	1000	7 US-11-266-748A-200612	Sequence 200612,
50	25.2	24.7	1062	7 US-11-217-529-849	Sequence 849, App
c 51	25.2	24.7	1089	7 US-11-266-748A-181702	Sequence 181702,
c 52	25.2	24.7	1114	7 US-11-266-748A-254692	Sequence 254692,
c 53	25.2	24.7	1114	7 US-11-266-748A-277130	Sequence 277130,
54	25.2	24.7	1114	7 US-11-266-748A-315209	Sequence 315209,
c 55	25.2	24.7	1233	7 US-11-266-748A-249171	Sequence 249171,
c 56	25.2	24.7	1235	7 US-11-266-748A-188440	Sequence 188440,
c 57	25.2	24.7	1282	7 US-11-266-748A-25905	Sequence 25905, A
c 58	25.2	24.7	1471	7 US-11-266-748A-3809	Sequence 3809, Ap
c 59	25.2	24.7	3486	6 US-10-517-441-556	Sequence 556, App

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OM nucleic - nucleic search, using sw model

Run on: July 1, 2006, 04:17:07 ; Search time 3700.06 Seconds
(without alignments)
1541.534 Million cell updates/sec

Title: US-10-630-536-4

Perfect score: 102

Sequence: 1 atttcccaccaatcaacgat.....tggacataaacatgaacatgg 102

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : EST:
1: gb_est1:
2: gb_est3:
3: gb_est4:
4: gb_est5:
5: gb_est6:
6: gb_htc:
7: gb_est2:
8: gb_est7:
9: gb_est8:
10: gb_est9:
11: gb_gss1:
12: gb_gss2:
13: gb_gss3:
14: gb_gss4:

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Score	Query Match	Length	DB	ID	Description
1	34.4	33.7	858	12	CC516020	CC516020 CH240_361
2	32.6	32.0	781	10	DV571328	DV571328 0058P0009
3	32.4	31.8	352	1	AA483240	AA483240 ne87h09.s
c 4	32.2	31.6	420	11	AQ132470	AQ132470 HS_3003_A
c 5	32	31.4	358	4	BX117527	BX117527 BX117527
c 6	31.8	31.2	741	11	BH920547	BH920547 odh72g09.
c 7	31.6	31.0	583	12	CE765576	CE765576 tigr-gss-
c 8	31.6	31.0	730	3	BU007004	BU007004 QGH13A24.
9	31.6	31.0	885	10	DV000824	DV000824 CNB209-D0
10	31.6	31.0	963	10	DW031234	DW031234 CFW210-C0
11	31.6	31.0	1070	10	DW671063	DW671063 CNB363-C1
12	31.6	31.0	1077	9	DN715926	DN715926 CNB11-H12
13	31.6	31.0	1138	10	DW664718	DW664718 CNB327-C0
14	31.6	31.0	1211	9	DN713155	DN713155 CNB06-D06
15	31.6	31.0	1393	9	DN687169	DN687169 CGX51-C11
c 16	31.4	30.8	417	4	BY266232	BY266232 BY266232
17	31.4	30.8	487	3	BQ488932	BQ488932 30-E9135-
18	31.4	30.8	572	11	AQ771527	AQ771527 HS_5399_A
c 19	31.4	30.8	659	12	CE683008	CE683008 tigr-gss-
20	31.4	30.8	850	8	CV301701	CV301701 MM12_H02
c 21	31.2	30.6	203	1	AV264282	AV264282 AV264282
22	31.2	30.6	710	11	AZ261111	AZ261111 RPCI-23-1
23	31.2	30.6	766	10	DR814197	DR814197 ZM_BFb004
24	31.2	30.6	788	14	DU654335	DU654335 OG_ABa005
25	31.2	30.6	791	2	BG501875	BG501875 602548974
26	31.2	30.6	798	9	DB293067	DB293067 DB293067
c 27	31.2	30.6	873	14	CR180171	CR180171 Forward s
c 28	31.2	30.6	1133	14	AG604607	AG604607 Mus muscu
c 29	30.8	30.2	593	5	CK876164	CK876164 SGP137428
c 30	30.8	30.2	745	3	BQ853453	BQ853453 QGB20I21.
c 31	30.8	30.2	860	12	CL098155	CL098155 ISB1-3007
32	30.8	30.2	867	1	AJ821715	AJ821715 AJ821715
c 33	30.8	30.2	877	10	DT749554	DT749554 EST118340
c 34	30.6	30.0	513	9	DN777882	DN777882 E5778 [C2
35	30.6	30.0	634	3	BW273512	BW273512 BW273512
36	30.6	30.0	644	5	CK534132	CK534132 rswgb0_00
c 37	30.6	30.0	702	3	BQ510748	BQ510748 EST618163
38	30.6	30.0	722	14	AG162641	AG162641 Pan trogl
c 39	30.4	29.8	198	14	BX964864	BX964864 Forward s
40	30.2	29.6	344	7	AW860820	AW860820 QV0-CT038
41	30.2	29.6	669	14	AG048006	AG048006 Pan trogl
42	30.2	29.6	730	10	DT561959	DT561959 EST107259
c 43	30	29.4	515	13	CZ552456	CZ552456 M0002497
44	30	29.4	720	11	BH932160	BH932160 odh58g08.
c 45	30	29.4	834	13	CW704484	CW704484 AIAA-aaa8
c 46	30	29.4	1097	1	AL534616	AL534616 AL534616
47	30	29.4	1497	2	BF788820	BF788820 602110529
c 48	29.8	29.2	384	13	CL887940	CL887940 abf87c05.
c 49	29.8	29.2	540	4	CB396886	CB396886 OSTR180H4
c 50	29.8	29.2	643	14	CR076760	CR076760 Forward s
c 51	29.8	29.2	659	11	AZ226184	AZ226184 RPCI-23-9
52	29.8	29.2	661	4	CA118151	CA118151 SCBGLR108
53	29.8	29.2	663	12	CC154488	CC154488 CSU-K34.1

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OM nucleic - nucleic search, using sw model

Run on: July 1, 2006, 03:55:42 ; Search time 357.646 Seconds
(without alignments)
4291.222 Million cell updates/sec

Title: US-10-630-536-5

Perfect score: 24

Sequence: 1 atttgtcggaaaggtcgcagtgaga 24

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : GenEmbl:
1: gb_env:
2: gb_pat:
3: gb_ph:
4: gb_pl:
5: gb_pr:
6: gb_ro:
7: gb_sts:
8: gb_sy:
9: gb_un:
10: gb_vi:
11: gb_ov:
12: gb_htg:
13: gb_in:
14: gb_om:
15: gb_ba:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query				Description
			Match	Length	DB	ID	
	1	24	100.0	24	2	CS001824	CS001824 Sequence
	2	24	100.0	147	2	CS001827	CS001827 Sequence
	3	24	100.0	96210	15	YPPMT1	AL117211 Yersinia
	4	24	100.0	100984	15	AF053947	AF053947 Yersinia
c	5	24	100.0	100990	2	AR487637	AR487637 Sequence
c	6	24	100.0	100990	15	AF074611	AF074611 Yersinia
	7	24	100.0	106516	15	STYPPHCM2	AL513384 Salmonell
	8	24	100.0	106642	15	AE017045	AE017045 Yersinia
	9	24	100.0	137036	15	AJ698720	AJ698720 Yersinia
c	10	19.2	80.0	198282	12	CT025723	CT025723 Drosophil
c	11	18.2	75.8	1014	6	AY336501	AY336501 Mus muscu
	12	18.2	75.8	1954	6	BC043679	BC043679 Mus muscu
c	13	18.2	75.8	2446	13	AY095069	AY095069 Drosophil
c	14	18.2	75.8	3461	2	CQ578330	CQ578330 Sequence
	15	18.2	75.8	3502	6	MUSGTPAAP	D11374 Mus musculu
	16	18.2	75.8	3519	2	AR052339	AR052339 Sequence
	17	18.2	75.8	3519	2	AR093112	AR093112 Sequence
	18	18.2	75.8	3519	2	E11890	E11890 cDNA encodi
	19	18.2	75.8	3519	2	AR214171	AR214171 Sequence
	20	18.2	75.8	3569	6	BC054824	BC054824 Mus muscu
	21	18.2	75.8	3741	6	AK220472	AK220472 Mus muscu
	22	18.2	75.8	6645	2	AR052341	AR052341 Sequence
	23	18.2	75.8	6645	2	AR093114	AR093114 Sequence
	24	18.2	75.8	6645	2	E11892	E11892 DNA encodin
	25	18.2	75.8	6645	2	AR214173	AR214173 Sequence
	26	18.2	75.8	12432	6	D87849	D87849 Mus musculu
c	27	18.2	75.8	34159	13	DMC165H7	AL009188 Drosophil
c	28	18.2	75.8	38591	13	CEC54E10	Z81487 Caenorhabdi
c	29	18.2	75.8	42473	12	AC020093	AC020093 Drosophil
	30	18.2	75.8	50531	5	AC145467	AC145467 Pan trogl
c	31	18.2	75.8	87740	13	AE003417_3	Continuation (4 of
c	32	18.2	75.8	117049	5	AC018987	AC018987 Homo sapi
c	33	18.2	75.8	118572	5	AL133408	AL133408 Human DNA
	34	18.2	75.8	163878	6	AC134563	AC134563 Mus muscu
c	35	18.2	75.8	168639	5	AC021818	AC021818 Homo sapi
c	36	18.2	75.8	170186	13	AC105774	AC105774 Drosophil
	37	18.2	75.8	170795	12	AC021346	AC021346 Homo sapi
	38	18.2	75.8	171990	6	AC117240	AC117240 Mus muscu
	39	18.2	75.8	174752	5	AC146075	AC146075 Pan trogl
	40	18.2	75.8	192074	6	AL840639	AL840639 Mouse DNA
c	41	18.2	75.8	200896	6	AC159251	AC159251 Mus muscu
	42	18.2	75.8	243976	6	AC159193	AC159193 Mus muscu
c	43	17.8	74.2	4843	5	AB035196	AB035196 Homo sapi
	44	17.8	74.2	6154	15	AF337952	AF337952 Azoarcus
	45	17.8	74.2	7037	2	AX344372	AX344372 Sequence
c	46	17.8	74.2	105321	5	AL928711	AL928711 Human DNA
	47	17.8	74.2	110000	12	CT005250_0	CT005250 Leishmani
c	48	17.8	74.2	110000	15	CR555306_13	Continuation (14 o
	49	17.8	74.2	110000	15	AE017143_08	Continuation (9 of
	50	17.8	74.2	124581	5	BX649364	BX649364 Human DNA
	51	17.8	74.2	136088	5	AL139426	AL139426 Human DNA
c	52	17.8	74.2	173910	5	BX855602	BX855602 Human DNA
c	53	17.8	74.2	186829	5	BX640519	BX640519 Human DNA
	54	17.6	73.3	633	7	BV279472	BV279472 S232P6452
	55	17.6	73.3	667	7	BV638707	BV638707 S216P6176
	56	17.6	73.3	2656	13	AF541879	AF541879 Branchios

SCORE Search Results Details for Application 10630536 and Search Result us-10-630-5.rng.

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OM nucleic - nucleic search, using sw model

Run on: July 1, 2006, 03:53:57 ; Search time 144.689 Seconds
 (without alignments)
 1156.508 Million cell updates/sec

Title: US-10-630-536-5

Perfect score: 24

Sequence: 1 atttgtcggaaaggtcgcagtgaga 24

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 150 summaries

Database : N_Geneseq_8:*
 1: geneseqn1980s:*
 2: geneseqn1990s:*
 3: geneseqn2000s:*
 4: geneseqn2001as:*
 5: geneseqn2001bs:*
 6: geneseqn2002as:*
 7: geneseqn2002bs:*
 8: geneseqn2003as:*
 9: geneseqn2003bs:*
 10: geneseqn2003cs:*
 11: geneseqn2003ds:*
 12: geneseqn2004as:*
 13: geneseqn2004bs:*
 14: geneseqn2005s:*
 15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query					Description
			Match	Length	DB	ID		
	1	24	100.0	24	14	ADV04870		Adv04870 Yersinia
	2	24	100.0	147	14	ADV04873		Adv04873 Yersinia
c	3	24	100.0	100990	12	ADJ94407		Adj94407 Yersinia
c	4	18.2	75.8	3461	4	ABL05898		Abl05898 Drosophil
	5	18.2	75.8	3500	2	AAT72782		Aat72782 Mouse int
	6	18.2	75.8	3519	2	AAT65000		Aat65000 Mouse cel
	7	18.2	75.8	6645	2	AAT65002		Aat65002 Mouse cel
	8	17.8	74.2	7037	6	ABK31376		Abk31376 Signal tr
c	9	17.6	73.3	10497	4	AAK67302		Aak67302 Human imm
	10	17.6	73.3	10497	4	AAK83166		Aak83166 Human imm
	11	17.6	73.3	171324	11	ACN43892		Acn43892 Mouse gen
	12	17.2	71.7	19639	2	AAX23524		Aax23524 O. longis
	13	17.2	71.7	76574	4	ABL03438		Abl03438 Drosophil
c	14	17.2	71.7	226215	11	ACN45146		Acn45146 Human gen
	15	16.8	70.0	364	5	AAF65355		Aaf65355 Novel hum
c	16	16.8	70.0	4296	4	ABL02046		Abl02046 Drosophil
c	17	16.8	70.0	4801	4	ABL26362		Ab126362 Drosophil
c	18	16.6	69.2	65	6	ABN53376		Abn53376 Mouse spl
c	19	16.6	69.2	100	8	ACD77600		Acd77600 E. coli K
c	20	16.6	69.2	100	8	ACD77601		Acd77601 E. coli K
	21	16.6	69.2	387	10	ACF69316		Acf69316 Photorhab
c	22	16.6	69.2	402	4	AAH84583		Aah84583 E. coli g
c	23	16.6	69.2	545	12	ADL88187		Adl88187 DNA up-re
c	24	16.6	69.2	545	12	ADL88186		Adl88186 DNA up-re
	25	16.6	69.2	834	12	ADO35971		Ado35971 Novel mou
	26	16.6	69.2	906	4	AAK83226		Aak83226 Human imm
c	27	16.6	69.2	998	6	ABT07198		Abt07198 Human CpG
	28	16.6	69.2	1167	13	ADX12937		Adx12937 Plant ful
	29	16.6	69.2	1280	12	ADI82283		Adi82283 Human DNA
	30	16.6	69.2	1720	2	AAQ78916		Aaq78916 Non-typab
	31	16.6	69.2	3599	11	ACN91978		Acn91978 Breast ca
	32	16.6	69.2	3864	13	ADS96669		Ads96669 Drosophil
	33	16.6	69.2	3907	14	ADY17893		Ady17893 DNA encod
	34	16.6	69.2	4003	4	ABL09841		Abl09841 Drosophil
c	35	16.6	69.2	4151	2	AAZ23663		Aaz23663 B. bassia
	36	16.6	69.2	4289	13	ADR07156		Adr07156 Full leng
	37	16.6	69.2	6237	6	ABL32359		Abl32359 Human imm
	38	16.6	69.2	6286	4	AAK83148		Aak83148 Human imm
	39	16.6	69.2	6751	4	AAK83163		Aak83163 Human imm
	40	16.6	69.2	6767	4	AAK83147		Aak83147 Human imm
	41	16.6	69.2	6943	4	AAK83198		Aak83198 Human imm
c	42	16.6	69.2	7004	13	ADT05477		Adt05477 Haemophil
c	43	16.6	69.2	7038	4	ABL09840		Abl09840 Drosophil
	44	16.6	69.2	7633	4	AAK83159		Aak83159 Human imm
	45	16.6	69.2	7906	4	AAK83154		Aak83154 Human imm
	46	16.6	69.2	9133	4	AAK83165		Aak83165 Human imm
	47	16.6	69.2	9217	4	AAK83151		Aak83151 Human imm
c	48	16.6	69.2	9439	4	AAK67312		Aak67312 Human imm
	49	16.6	69.2	9439	4	AAK83168		Aak83168 Human imm
	50	16.6	69.2	9832	4	AAK83150		Aak83150 Human imm
	51	16.6	69.2	11428	4	AAK83156		Aak83156 Human imm
	52	16.6	69.2	11744	4	AAK83160		Aak83160 Human imm
c	53	16.6	69.2	11853	4	AAK67297		Aak67297 Human imm
	54	16.6	69.2	11853	4	AAK83162		Aak83162 Human imm
	55	16.6	69.2	14258	4	AAK83210		Aak83210 Human imm
	56	16.6	69.2	14260	4	AAK83183		Aak83183 Human imm

SCORE Search Results Details for Application 10630536 and Search Result us-10-630-536-5.

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OM nucleic - nucleic search, using sw model

Run on: July 1, 2006, 04:28:37 ; Search time 29.4545 Seconds
(without alignments)
1524.607 Million cell updates/sec

Title: US-10-630-536-5
Perfect score: 24
Sequence: 1 atttgcggaaaggtcgcagtgaga 24

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : Issued_Patents_NA:
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3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:
4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:
5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:
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9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	SUMMARIES			
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					Description

c	1	24	100.0	100990	3	US-09-409-800B-2	Sequence 2, Appli
	2	18.2	75.8	3519	2	US-08-380-403A-1	Sequence 1, Appli
	3	18.2	75.8	3519	2	US-08-895-628-1	Sequence 1, Appli
	4	18.2	75.8	3519	3	US-08-895-810D-1	Sequence 1, Appli
	5	18.2	75.8	6645	2	US-08-380-403A-4	Sequence 4, Appli
	6	18.2	75.8	6645	2	US-08-895-628-4	Sequence 4, Appli
	7	18.2	75.8	6645	3	US-08-895-810D-4	Sequence 4, Appli
c	8	16.6	69.2	402	3	US-09-711-164-211	Sequence 211, App
c	9	16.6	69.2	601	3	US-09-949-016-87151	Sequence 87151, A
c	10	16.6	69.2	601	3	US-09-949-016-109809	Sequence 109809,
	11	16.6	69.2	601	3	US-09-949-016-152778	Sequence 152778,
	12	16.6	69.2	601	3	US-09-949-016-152779	Sequence 152779,
c	13	16.6	69.2	998	3	US-09-775-398-15	Sequence 15, Appli
	14	16.6	69.2	1720	2	US-08-457-997B-1	Sequence 1, Appli
	15	16.6	69.2	1720	3	US-08-467-722A-1	Sequence 1, Appli
	16	16.6	69.2	1720	3	US-09-451-184-1	Sequence 1, Appli
c	17	16.6	69.2	7649	3	US-09-949-016-16033	Sequence 16033, A
c	18	16.6	69.2	72049	3	US-09-544-398B-9	Sequence 9, Appli
c	19	16.6	69.2	72049	3	US-09-543-771B-9	Sequence 9, Appli
	20	16.6	69.2	92681	3	US-09-949-016-14772	Sequence 14772, A
c	21	16.6	69.2	140844	3	US-09-949-016-14199	Sequence 14199, A
	22	16.2	67.5	576	3	US-09-252-991A-4866	Sequence 4866, Ap
	23	16.2	67.5	768	3	US-09-252-991A-12489	Sequence 12489, A
	24	16.2	67.5	1069	3	US-09-270-767-11416	Sequence 11416, A
	25	16.2	67.5	1230	3	US-09-134-000C-2763	Sequence 2763, Ap
c	26	16.2	67.5	1260	3	US-09-252-991A-4852	Sequence 4852, Ap
c	27	16.2	67.5	2492	3	US-09-973-278-708	Sequence 708, App
	28	16.2	67.5	153866	3	US-09-949-016-16919	Sequence 16919, A
c	29	16	66.7	700	3	US-09-735-271-761	Sequence 761, App
c	30	16	66.7	1075	3	US-09-270-767-28307	Sequence 28307, A
c	31	16	66.7	1324	3	US-09-270-767-12525	Sequence 12525, A
	32	16	66.7	54550	3	US-10-327-189-42	Sequence 42, Appli
c	33	16	66.7	276687	3	US-09-949-016-13840	Sequence 13840, A
	34	15.8	65.8	206	3	US-09-513-999C-28375	Sequence 28375, A
	35	15.8	65.8	601	3	US-09-949-016-53929	Sequence 53929, A
	36	15.8	65.8	601	3	US-09-949-016-53930	Sequence 53930, A
	37	15.8	65.8	601	3	US-09-949-016-53931	Sequence 53931, A
c	38	15.8	65.8	601	3	US-09-949-001-227	Sequence 227, App
c	39	15.8	65.8	601	3	US-09-949-001-501	Sequence 501, App
	40	15.8	65.8	601	3	US-09-949-002-2320	Sequence 2320, Ap
	41	15.8	65.8	601	3	US-09-949-002-4920	Sequence 4920, Ap
	42	15.8	65.8	1172	3	US-09-902-540-6171	Sequence 6171, Ap
c	43	15.8	65.8	1621	3	US-09-902-540-309	Sequence 309, App
	44	15.8	65.8	2139	3	US-09-949-002-142	Sequence 142, App
	45	15.8	65.8	4173	3	US-09-949-002-61	Sequence 61, Appl
c	46	15.8	65.8	36148	3	US-09-949-016-12969	Sequence 12969, A
	47	15.8	65.8	70313	3	US-09-949-002-714	Sequence 714, App
	48	15.8	65.8	72347	3	US-09-949-002-633	Sequence 633, App
	49	15.8	65.8	75176	3	US-09-949-016-13300	Sequence 13300, A
c	50	15.8	65.8	192302	3	US-09-949-016-15270	Sequence 15270, A
c	51	15.8	65.8	246230	3	US-09-949-016-17019	Sequence 17019, A
c	52	15.8	65.8	246230	3	US-09-949-016-17020	Sequence 17020, A
c	53	15.8	65.8	246230	3	US-09-949-016-17021	Sequence 17021, A
c	54	15.8	65.8	246230	3	US-09-949-016-17022	Sequence 17022, A
c	55	15.8	65.8	312957	3	US-09-949-001-31	Sequence 31, Appl
c	56	15.8	65.8	312972	3	US-09-949-001-34	Sequence 34, Appl
c	57	15.8	65.8	325791	3	US-09-768-185A-1	Sequence 1, Appli
c	58	15.6	65.0	144	3	US-09-513-999C-29481	Sequence 29481, A
	59	15.6	65.0	424	3	US-09-513-999C-9813	Sequence 9813, Ap
c	60	15.6	65.0	460	2	US-08-967-101-48	Sequence 48, Appl

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OM nucleic - nucleic search, using sw model

Run on: July 1, 2006, 04:38:10 ; Search time 334.105 Seconds
(without alignments)
882.666 Million cell updates/sec

Title: US-10-630-536-5
Perfect score: 24
Sequence: 1 atttgtcgaaaggtcgcagtgaga 24

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : Published_Applications_NA_Main:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	24	100.0	24	11	US-10-630-536-5		Sequence 5, Appli
2	24	100.0	147	11	US-10-630-536-8		Sequence 8, Appli
3	18.8	78.3	600	10	US-10-972-079-79803		Sequence 79803, A
c 4	18.2	75.8	3461	13	US-11-097-143-6088		Sequence 6088, Ap
c 5	17.6	73.3	201	9	US-10-741-600-59349		Sequence 59349, A
6	17.6	73.3	581	4	US-09-925-065A-636311		Sequence 636311,
7	17.6	73.3	581	4	US-09-925-065A-636312		Sequence 636312,
8	17.6	73.3	581	5	US-09-925-065A-636311		Sequence 636311,
9	17.6	73.3	581	5	US-09-925-065A-636312		Sequence 636312,
c 10	17.6	73.3	818	6	US-10-027-632-325318		Sequence 325318,
c 11	17.6	73.3	818	7	US-10-027-632-325318		Sequence 325318,
12	17.6	73.3	171324	6	US-10-087-192-67		Sequence 67, Appl
c 13	17.6	73.3	385320	9	US-10-741-600-17796		Sequence 17796, A
c 14	17.6	73.3	1080000	10	US-10-928-446A-1		Sequence 1, Appli
c 15	17.6	73.3	1080000	10	US-10-928-446A-181		Sequence 181, App
c 16	17.6	73.3	1080000	10	US-10-928-446A-183		Sequence 183, App
c 17	17.6	73.3	1080000	10	US-10-928-446A-185		Sequence 185, App
c 18	17.6	73.3	1080000	10	US-10-928-446A-187		Sequence 187, App
c 19	17.6	73.3	1080000	10	US-10-928-446A-189		Sequence 189, App
c 20	17.6	73.3	1080000	10	US-10-928-446A-191		Sequence 191, App
c 21	17.6	73.3	1080000	10	US-10-928-446A-193		Sequence 193, App
c 22	17.6	73.3	1080000	10	US-10-928-446A-195		Sequence 195, App
c 23	17.6	73.3	1080000	10	US-10-928-446A-197		Sequence 197, App
c 24	17.6	73.3	1080000	10	US-10-928-446A-199		Sequence 199, App
c 25	17.6	73.3	1080000	10	US-10-928-446A-201		Sequence 201, App
c 26	17.4	72.5	25	9	US-10-719-900-404868		Sequence 404868,
c 27	17.2	71.7	25	9	US-10-719-900-134888		Sequence 134888,
c 28	17.2	71.7	427	4	US-09-925-065A-839028		Sequence 839028,
c 29	17.2	71.7	427	5	US-09-925-065A-839028		Sequence 839028,
30	17.2	71.7	472	4	US-09-925-065A-269771		Sequence 269771,
31	17.2	71.7	472	4	US-09-925-065A-269772		Sequence 269772,
32	17.2	71.7	472	4	US-09-925-065A-269773		Sequence 269773,
33	17.2	71.7	472	5	US-09-925-065A-269771		Sequence 269771,
34	17.2	71.7	472	5	US-09-925-065A-269772		Sequence 269772,
35	17.2	71.7	472	5	US-09-925-065A-269773		Sequence 269773,
36	17.2	71.7	479	12	US-10-301-480-347316		Sequence 347316,
37	17.2	71.7	479	12	US-10-301-480-347317		Sequence 347317,
38	17.2	71.7	479	12	US-10-301-480-347318		Sequence 347318,
39	17.2	71.7	479	12	US-10-301-480-960725		Sequence 960725,
40	17.2	71.7	479	12	US-10-301-480-960726		Sequence 960726,
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c 43	17.2	71.7	529	5	US-09-925-065A-325085		Sequence 325085,
c 44	17.2	71.7	593	4	US-09-925-065A-570380		Sequence 570380,
c 45	17.2	71.7	593	4	US-09-925-065A-570381		Sequence 570381,
c 46	17.2	71.7	593	5	US-09-925-065A-570380		Sequence 570380,
c 47	17.2	71.7	593	5	US-09-925-065A-570381		Sequence 570381,
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49	17.2	71.7	606	12	US-10-301-480-666732		Sequence 666732,
50	17.2	71.7	619	6	US-10-027-632-253142		Sequence 253142,
51	17.2	71.7	619	7	US-10-027-632-253142		Sequence 253142,

SCORE Search Results Details for Application 10630536 and Search Result us-10-630-536-5.rn

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OM nucleic - nucleic search, using sw model

Run on: July 1, 2006, 04:39:12 ; Search time 24.9187 Seconds
(without alignments)
1138.902 Million cell updates/sec

Title: US-10-630-536-5

Perfect score: 24

Sequence: 1 atttgtcggaaaggtcgcagtgaga 24

Scoring table: IDENTITY_NUC
Gapext 1.0 , Gapext 1.0

Searched: 809770 seqs, 591248006 residues

Total number of hits satisfying chosen parameters: 1619540

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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c	3	16.8	70.0	1485	7	US-11-266-748A-2939	Sequence 2939, Ap
c	4	16.8	70.0	1839	7	US-11-266-748A-259273	Sequence 259273,
	5	16.8	70.0	1839	7	US-11-266-748A-319790	Sequence 319790,
	6	16.6	69.2	496	7	US-11-266-748A-95692	Sequence 95692, A
	7	16.6	69.2	496	7	US-11-266-748A-113285	Sequence 113285,
c	8	16.6	69.2	496	7	US-11-266-748A-148503	Sequence 148503,
	9	16.6	69.2	822	7	US-11-266-748A-273220	Sequence 273220,
c	10	16.6	69.2	822	7	US-11-266-748A-333737	Sequence 333737,
	11	16.6	69.2	1505	6	US-10-449-902-4636	Sequence 4636, Ap
	12	16.6	69.2	1671	7	US-11-216-545-1388	Sequence 1388, Ap
c	13	16.6	69.2	1798	6	US-10-953-349-21708	Sequence 21708, A
	14	16.6	69.2	2091	6	US-10-449-902-20807	Sequence 20807, A
c	15	16.6	69.2	124048	7	US-11-266-748A-59707	Sequence 59707, A
c	16	16.6	69.2	156641	7	US-11-266-748A-61706	Sequence 61706, A
c	17	16.2	67.5	400	7	US-11-266-748A-219541	Sequence 219541,
	18	16.2	67.5	714	7	US-11-266-748A-418375	Sequence 418375,
	19	16	66.7	462	7	US-11-266-748A-270178	Sequence 270178,
c	20	16	66.7	462	7	US-11-266-748A-330695	Sequence 330695,
	21	16	66.7	638	7	US-11-266-748A-51873	Sequence 51873, A
c	22	16	66.7	1000	7	US-11-266-748A-204106	Sequence 204106,
	23	16	66.7	1233	7	US-11-266-748A-71926	Sequence 71926, A
	24	16	66.7	1233	7	US-11-266-748A-106932	Sequence 106932,
c	25	16	66.7	1233	7	US-11-266-748A-124737	Sequence 124737,
	26	16	66.7	1834	7	US-11-293-697-2209	Sequence 2209, Ap
	27	16	66.7	2391	7	US-11-217-529-2137	Sequence 2137, Ap
	28	16	66.7	2818	6	US-10-449-902-14998	Sequence 14998, A
	29	16	66.7	54550	7	US-11-318-813-42	Sequence 42, Appl
c	30	15.8	65.8	224	7	US-11-266-748A-427565	Sequence 427565,
	31	15.8	65.8	477	7	US-11-217-529-3681	Sequence 3681, Ap
c	32	15.8	65.8	872	7	US-11-266-748A-356713	Sequence 356713,
c	33	15.8	65.8	872	7	US-11-266-748A-386049	Sequence 386049,
	34	15.8	65.8	872	7	US-11-266-748A-440092	Sequence 440092,
	35	15.8	65.8	888	7	US-11-266-748A-49215	Sequence 49215, A
	36	15.8	65.8	888	7	US-11-266-748A-215068	Sequence 215068,
c	37	15.8	65.8	1000	7	US-11-266-748A-295338	Sequence 295338,
	38	15.8	65.8	1000	7	US-11-266-748A-346767	Sequence 346767,
c	39	15.8	65.8	1000	7	US-11-266-748A-408092	Sequence 408092,
	40	15.8	65.8	1000	7	US-11-266-748A-479138	Sequence 479138,
	41	15.8	65.8	1344	7	US-11-266-748A-180079	Sequence 180079,
	42	15.8	65.8	1344	7	US-11-266-748A-191166	Sequence 191166,
c	43	15.8	65.8	1344	7	US-11-266-748A-240222	Sequence 240222,
	44	15.8	65.8	1875	6	US-10-953-349-23838	Sequence 23838, A
	45	15.8	65.8	4345	7	US-11-266-748A-27300	Sequence 27300, A
	46	15.8	65.8	126068	7	US-11-257-817-31	Sequence 31, Appl
c	47	15.6	65.0	396	7	US-11-266-748A-428564	Sequence 428564,
c	48	15.6	65.0	402	7	US-11-266-748A-34589	Sequence 34589, A
c	49	15.6	65.0	488	7	US-11-266-748A-380591	Sequence 380591,
	50	15.6	65.0	488	7	US-11-266-748A-463970	Sequence 463970,
c	51	15.6	65.0	839	7	US-11-266-748A-214593	Sequence 214593,
	52	15.6	65.0	839	7	US-11-266-748A-237144	Sequence 237144,
	53	15.6	65.0	1000	7	US-11-266-748A-202805	Sequence 202805,
	54	15.6	65.0	1000	7	US-11-266-748A-223076	Sequence 223076,
c	55	15.6	65.0	1000	7	US-11-266-748A-282724	Sequence 282724,
	56	15.6	65.0	1000	7	US-11-266-748A-290128	Sequence 290128,
	57	15.6	65.0	1000	7	US-11-266-748A-309364	Sequence 309364,
c	58	15.6	65.0	1000	7	US-11-266-748A-341557	Sequence 341557,
c	59	15.6	65.0	1000	7	US-11-266-748A-392248	Sequence 392248,
	60	15.6	65.0	1000	7	US-11-266-748A-401301	Sequence 401301,
c	61	15.6	65.0	1000	7	US-11-266-748A-472347	Sequence 472347,
	62	15.6	65.0	1000	7	US-11-266-748A-482966	Sequence 482966,

SCORE Search Results Details for Application 10630536 and Search Result us-10-630-536-5.rst.

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OM nucleic - nucleic search, using sw model

Run on: July 1, 2006, 04:17:07 ; Search time 870.603 Seconds
(without alignments)
1541.534 Million cell updates/sec

Title: US-10-630-536-5
Perfect score: 24
Sequence: 1 atttgtcggaaagggtcgacgtgaga 24

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : EST:
1: gb_est1:
2: gb_est3:
3: gb_est4:
4: gb_est5:
5: gb_est6:
6: gb_htc:
7: gb_est2:
8: gb_est7:
9: gb_est8:
10: gb_est9:
11: gb_gss1:
12: gb_gss2:
13: gb_gss3:
14: gb_gss4:

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
	1	19.2	80.0	412	7	BF133335
	2	19.2	80.0	766	12	CC313955
c	3	18.8	78.3	860	7	BE961221
	4	18.2	75.8	250	10	W43945
	5	18.2	75.8	431	1	AA646761
	6	18.2	75.8	439	2	BG145962
	7	18.2	75.8	468	10	W83596
	8	18.2	75.8	499	1	AI182978
	9	18.2	75.8	546	1	AI182158
	10	18.2	75.8	548	1	AA475649
c	11	18.2	75.8	549	3	BU670475
	12	18.2	75.8	569	1	AA272920
	13	18.2	75.8	573	1	AA273284
	14	18.2	75.8	588	2	BG228327
	15	18.2	75.8	596	5	CK133093
	16	18.2	75.8	644	10	W57213
	17	18.2	75.8	646	1	AI154692
c	18	18.2	75.8	647	3	BQ174962
	19	18.2	75.8	649	7	AW476530
	20	18.2	75.8	668	2	BI082542
	21	18.2	75.8	686	1	AV088479
c	22	18.2	75.8	829	13	DU091573
	23	18.2	75.8	843	2	BG975564
	24	18.2	75.8	856	4	CA977500
	25	18.2	75.8	998	7	BF124739
	26	18.2	75.8	999	14	CNS06ZW6
c	27	18.2	75.8	1160	6	AK005865
	28	18.2	75.8	2802	6	AK028151
	29	18.2	75.8	3457	6	AK169945
	30	18.2	75.8	3520	6	AK149669
	31	18.2	75.8	3538	6	AK137578
	32	18.2	75.8	3813	6	AK156280
c	33	17.8	74.2	655	11	BZ116006
	34	17.8	74.2	659	11	BH887754
c	35	17.8	74.2	667	7	BB095304
c	36	17.8	74.2	747	8	CN039648
c	37	17.8	74.2	800	2	BG195843
c	38	17.8	74.2	810	13	DU119015
c	39	17.8	74.2	812	10	DT829517
c	40	17.8	74.2	822	10	DT857579
c	41	17.8	74.2	949	5	CK404641
c	42	17.8	74.2	1394	12	CC258210
c	43	17.6	73.3	262	14	CR089939
c	44	17.6	73.3	294	8	CV427205
c	45	17.6	73.3	406	8	CO593747
c	46	17.6	73.3	427	12	CE438745
c	47	17.6	73.3	453	3	BU830938
c	48	17.6	73.3	513	8	CO616233
c	49	17.6	73.3	522	2	BF963391
c	50	17.6	73.3	542	8	CO688501
c	51	17.6	73.3	548	11	AQ484393
c	52	17.6	73.3	585	1	AL683669
c	53	17.6	73.3	609	2	BG348685

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OM nucleic - nucleic search, using sw model

Run on: July 1, 2006, 03:55:42 ; Search time 342.744 Seconds
 (without alignments)
 4291.222 Million cell updates/sec

Title: US-10-630-536-6

Perfect score: 23

Sequence: 1 cgtcgatgactttctgacggcac 23

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 150 summaries

Database : GenEmbl:
 1: gb_env:
 2: gb_pat:
 3: gb_ph:
 4: gb_pl:
 5: gb_pr:
 6: gb_ro:
 7: gb_sts:
 8: gb_sy:
 9: gb_un:
 10: gb_vi:
 11: gb_ov:
 12: gb_htg:
 13: gb_in:
 14: gb_om:
 15: gb_ba:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Query					Description
		Score	Match	Length	DB	ID	
	1	23	100.0	23	2	CS001825	CS001825 Sequence
c	2	23	100.0	147	2	CS001827	CS001827 Sequence
c	3	23	100.0	96210	15	YPPMT1	AL117211 Yersinia
c	4	23	100.0	100984	15	AF053947	AF053947 Yersinia
	5	23	100.0	100990	2	AR487637	AR487637 Sequence
	6	23	100.0	100990	15	AF074611	AF074611 Yersinia
c	7	23	100.0	106516	15	STYPPHCM2	AL513384 Salmonell
c	8	23	100.0	106642	15	AE017045	AE017045 Yersinia
c	9	23	100.0	137036	15	AJ698720	AJ698720 Yersinia
	10	19.8	86.1	110000	4	AP008216_068	Continuation (69 o
	11	19.8	86.1	110000	4	AE016959_068	Continuation (69 o
	12	19.8	86.1	137568	4	AC093178	AC093178 Oryza sat
c	13	19.4	84.3	12026	15	AE005109	AE005109 Halobacte
	14	19.4	84.3	189230	12	AC120836	AC120836 Mus muscu
	15	19.4	84.3	209356	6	AL806525	AL806525 Mouse DNA
c	16	18.4	80.0	103975	4	AY702979	AY702979 Capsicum
	17	18.2	79.1	110000	4	AP008212_114	Continuation (115
	18	18.2	79.1	110000	4	AP008207_032	Continuation (33 o
	19	18.2	79.1	133019	4	AP006054	AP006054 Oryza sat
	20	18.2	79.1	167761	4	AP003209	AP003209 Oryza sat
c	21	17.8	77.4	8524	15	AB100500	AB100500 Selenomon
	22	17.8	77.4	44117	13	AY190946	AY190946 Drosophil
	23	17.8	77.4	110000	4	CR382131_13	Continuation (14 o
c	24	17.8	77.4	110000	12	CT005271_16	Continuation (17 o
c	25	17.8	77.4	110000	15	AE004969_06	Continuation (7 of
	26	17.8	77.4	110000	15	CP000100_08	Continuation (9 of
c	27	17.8	77.4	110000	15	AP008231_07	Continuation (8 of
c	28	17.4	75.7	1432	4	AK107315	AK107315 Oryza sat
	29	17.4	75.7	110000	15	BA000040_53	Continuation (54 o
	30	17.2	74.8	738	2	AX436604	AX436604 Sequence
c	31	17.2	74.8	9680	15	AY972822	AY972822 Rhodother
c	32	17.2	74.8	56390	2	CQ603410	CQ603410 Sequence
c	33	17.2	74.8	64799	13	CP000212	CP000212 Drosophil
c	34	17.2	74.8	66833	12	AC101655	AC101655 Mus muscu
	35	17.2	74.8	110000	4	AP008213_076	Continuation (77 o
	36	17.2	74.8	110000	4	AP008218_245	Continuation (246
	37	17.2	74.8	110000	12	AP006491_0	AP006491 Cyanidios
	38	17.2	74.8	110000	15	AE002098_14	Continuation (15 o
c	39	17.2	74.8	110000	15	AE004969_07	Continuation (8 of
c	40	17.2	74.8	110000	15	CP000086_20	Continuation (21 o
c	41	17.2	74.8	110000	15	CP000142_00	CP000142 Pelobacte
c	42	17.2	74.8	110000	15	RME591985_13	Continuation (14 o
	43	17.2	74.8	110807	6	AP003184	AP003184 Mus muscu
	44	17.2	74.8	135862	6	AC132576	AC132576 Mus muscu
	45	17.2	74.8	143895	4	CNS08CD6	AL954852 Oryza sat
	46	17.2	74.8	152191	4	AP005194	AP005194 Oryza sat
c	47	17.2	74.8	155094	12	AC122080	AC122080 Rattus no
	48	17.2	74.8	157990	12	AC137311	AC137311 Rattus no
	49	17.2	74.8	165518	13	AC091226	AC091226 Drosophil
c	50	17.2	74.8	171749	6	AC134437	AC134437 Mus muscu
c	51	17.2	74.8	177466	15	AE001826	AE001826 Deinococc
	52	17.2	74.8	191909	12	AC161801	AC161801 Mus muscu
c	53	17.2	74.8	193074	12	AC017576	AC017576 Drosophil
	54	17.2	74.8	203416	6	AC125352	AC125352 Mus muscu
c	55	17.2	74.8	217713	12	AC119007	AC119007 Rattus no
	56	17.2	74.8	238355	12	AC113917	AC113917 Rattus no

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Result us-10-630-536-6.rng.

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OM nucleic - nucleic search, using sw model

Run on: July 1, 2006, 03:53:57 ; Search time 138.66 Seconds
(without alignments)
1156.508 Million cell updates/sec

Title: US-10-630-536-6

Perfect score: 23

Sequence: 1 cgtcgatgactttctgacggcac 23

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : N_Geneseq_8:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Query					Description
		Score	Match	Length	DB	ID	
	1	23	100.0	23	14	ADV04871	Adv04871 Yersinia
c	2	23	100.0	147	14	ADV04873	Adv04873 Yersinia
	3	23	100.0	100990	12	ADJ94407	Adj94407 Yersinia
	4	17.8	77.4	1443	8	ACA41226	Aca41226 Prokaryot
	5	17.8	77.4	1443	10	ABZ39903	Abz39903 N. gonorr
	6	17.2	74.8	738	6	ABK77728	Abk77728 Bacillus
	7	17.2	74.8	1974	8	ACA40983	Aca40983 Prokaryot
	8	17.2	74.8	1974	10	ABZ40096	Abz40096 N. gonorr
	9	17.2	74.8	1977	8	ACA41918	Aca41918 Prokaryot
c	10	17.2	74.8	48275	3	AAA81501	Aaa81501 N. mening
c	11	17.2	74.8	56390	4	ABL22618	AbL22618 Drosophil
	12	17.2	74.8	110000	3	AAA81489_0	Aaa81489 N. mening
	13	17.2	74.8	349980	3	AAF21610	Aaf21610 Neisseria
	14	16.8	73.0	1404	6	ABN67300	Abn67300 Streptoco
	15	16.8	73.0	1404	6	ABN70378	Abn70378 Streptoco
	16	16.8	73.0	31122	2	AAQ40706	Aaq40706 Bacillus
c	17	16.8	73.0	110000	6	ABN71527_17	Continuation (18 o
c	18	16.8	73.0	110000	6	ABN71527_18	Continuation (19 o
	19	16.8	73.0	349980	6	ABQ81847	Abq81847 Bifidobac
c	20	16.6	72.2	25	9	ACK05770	Ack05770 Human mic
	21	16.6	72.2	30	13	ADS73313	Ads73313 Plant 3 R
c	22	16.6	72.2	333	6	ABN20453	Abn20453 Human ORF
c	23	16.6	72.2	337	6	ABN19524	Abn19524 Human ORF
c	24	16.6	72.2	363	5	ABV06373	Abv06373 Human pro
	25	16.6	72.2	378	11	ABD06655	Abd06655 Pseudomon
c	26	16.6	72.2	465	5	AAS79166	Aas79166 DNA encod
c	27	16.6	72.2	513	5	AAH65061	Aah65061 C glutami
c	28	16.6	72.2	636	14	AEB15370	Aeb15370 C glutami
c	29	16.6	72.2	636	14	AED72481	Aed72481 Corynebac
	30	16.6	72.2	834	12	ADO07789	Ado07789 Fly polyn
	31	16.6	72.2	981	11	ABD06627	Abd06627 Pseudomon
	32	16.6	72.2	1159	4	ABL18289	AbL18289 Drosophil
c	33	16.6	72.2	1275	4	AAF29692	Aaf29692 P acnes 1
c	34	16.6	72.2	1275	12	ADJ34080	Adj34080 P. acnes
c	35	16.6	72.2	1278	12	ADJ34074	Adj34074 P. acnes
	36	16.6	72.2	1650	5	AAS89367	Aas89367 DNA encod
c	37	16.6	72.2	1988	13	ADX51497	Adx51497 Plant ful
c	38	16.6	72.2	2028	10	ADE58576	Ade58576 Human gen
c	39	16.6	72.2	2172	14	ACL69720	Acl69720 M. xanthu
c	40	16.6	72.2	5275	4	AAF29691	Aaf29691 P acnes 1
	41	16.6	72.2	5801	4	AAS59582	Aas59582 Propionib
	42	16.6	72.2	5801	8	ACF64511	Acf64511 Propionib
c	43	16.6	72.2	11301	14	ACL64583	Acl64583 M. xanthu
	44	16.6	72.2	16658	4	AAS59630	Aas59630 Propionib
	45	16.6	72.2	16658	8	ACF64559	Acf64559 Propionib
c	46	16.6	72.2	34361	4	ABL18288	AbL18288 Drosophil
	47	16.6	72.2	349980	5	AAH64966	Aah64966 C glutami
c	48	16.4	71.3	109	2	AAX56039	Aax56039 HIV-1 Gro
c	49	16.4	71.3	109	2	AAX37154	Aax37154 PCR prime
c	50	16.4	71.3	109	3	AAZ90265	Aaz90265 Synthetic
c	51	16.4	71.3	1125	2	AAX56076	Aax56076 HIV-1 Gro
c	52	16.4	71.3	1125	2	AAX37191	Aax37191 Recombina
c	53	16.4	71.3	1860	2	AAX56077	Aax56077 HIV-1 Gro
c	54	16.4	71.3	1860	2	AAX37192	Aax37192 Recombina
c	55	16.4	71.3	1860	3	AAZ90283	Aaz90283 HIV-1 gro
	56	16.4	71.3	4073	12	ADQ64993	Adq64993 Novel hum

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OM nucleic - nucleic search, using sw model

Run on: July 1, 2006, 04:28:37 ; Search time 28.2273 Seconds
(without alignments)
1524.607 Million cell updates/sec

Title: US-10-630-536-6

Perfect score: 23

Sequence: 1 cgtcgatgactttctgacggcac 23

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : Issued_Patents_NA:
1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%
	Query

No.	Score	Match	Length	DB	ID	Description
	23	100.0	100990	3	US-09-409-800B-2	Sequence 2, Appli
	17.2	74.8	738	5	US-09-974-300-5019	Sequence 5019, Ap
c 3	16.8	73.0	69909	3	US-09-949-016-13423	Sequence 13423, A
c 4	16.6	72.2	378	3	US-09-252-991A-5259	Sequence 5259, Ap
c 5	16.6	72.2	636	4	US-09-605-703B-2657	Sequence 2657, Ap
c 6	16.6	72.2	640	3	US-09-270-767-15249	Sequence 15249, A
c 7	16.6	72.2	981	3	US-09-252-991A-5231	Sequence 5231, Ap
c 8	16.6	72.2	1275	3	US-09-561-077C-60	Sequence 60, Appl
c 9	16.6	72.2	2172	3	US-09-902-540-6183	Sequence 6183, Ap
c 10	16.6	72.2	5275	3	US-09-561-077C-59	Sequence 59, Appl
c 11	16.6	72.2	11301	3	US-09-902-540-1046	Sequence 1046, Ap
c 12	16.4	71.3	109	2	US-08-912-129A-12	Sequence 12, Appl
c 13	16.4	71.3	109	3	US-08-911-824-12	Sequence 12, Appl
c 14	16.4	71.3	1125	2	US-08-912-129A-51	Sequence 51, Appl
c 15	16.4	71.3	1125	3	US-08-911-824-51	Sequence 51, Appl
c 16	16.4	71.3	1860	2	US-08-912-129A-53	Sequence 53, Appl
c 17	16.4	71.3	1860	3	US-08-911-824-53	Sequence 53, Appl
18	16.2	70.4	228	3	US-09-248-796A-4395	Sequence 4395, Ap
19	16.2	70.4	1008	3	US-09-106-075A-17	Sequence 17, Appl
20	16.2	70.4	1068	2	US-08-210-762E-18	Sequence 18, Appl
21	16.2	70.4	1191	2	US-08-210-762E-20	Sequence 20, Appl
22	16.2	70.4	1191	3	US-09-106-075A-20	Sequence 20, Appl
c 23	16.2	70.4	1215	3	US-09-489-039A-2312	Sequence 2312, Ap
24	16.2	70.4	1413	3	US-09-248-796A-4379	Sequence 4379, Ap
c 25	16.2	70.4	2334	3	US-09-248-796A-1911	Sequence 1911, Ap
26	16.2	70.4	101674	3	US-09-949-016-12033	Sequence 12033, A
27	15.8	68.7	2151	3	US-09-303-518D-111	Sequence 111, App
c 28	15.8	68.7	7029	5	US-10-261-481-1	Sequence 1, Appli
c 29	15.8	68.7	32155	3	US-08-311-731A-1	Sequence 1, Appli
30	15.8	68.7	4403765	3	US-09-103-840A-2	Sequence 2, Appli
31	15.8	68.7	4411529	3	US-09-103-840A-1	Sequence 1, Appli
c 32	15.6	67.8	582	3	US-09-252-991A-12907	Sequence 12907, A
33	15.6	67.8	601	3	US-09-949-016-200076	Sequence 200076,
34	15.6	67.8	805	3	US-09-270-767-9873	Sequence 9873, Ap
c 35	15.6	67.8	1128	3	US-09-902-540-7183	Sequence 7183, Ap
36	15.6	67.8	1149	3	US-09-303-518D-189	Sequence 189, App
37	15.6	67.8	1149	3	US-09-303-518D-191	Sequence 191, App
38	15.6	67.8	1275	3	US-09-107-532A-2687	Sequence 2687, Ap
39	15.6	67.8	4094	3	US-09-902-540-665	Sequence 665, App
40	15.6	67.8	22927	3	US-09-949-016-11849	Sequence 11849, A
41	15.6	67.8	22928	3	US-09-949-016-13071	Sequence 13071, A
42	15.6	67.8	36181	3	US-08-311-731A-120	Sequence 120, App
c 43	15.6	67.8	38653	3	US-09-922-445-1	Sequence 1, Appli
44	15.6	67.8	84296	3	US-09-949-016-17375	Sequence 17375, A
45	15.6	67.8	536165	3	US-09-214-808-1	Sequence 1, Appli
c 46	15.6	67.8	4403765	3	US-09-103-840A-2	Sequence 2, Appli
c 47	15.6	67.8	4411529	3	US-09-103-840A-1	Sequence 1, Appli
c 48	15.4	67.0	601	3	US-09-949-016-198698	Sequence 198698,
c 49	15.4	67.0	601	3	US-09-949-016-198699	Sequence 198699,
c 50	15.4	67.0	6944	3	US-09-949-016-3637	Sequence 3637, Ap
c 51	15.4	67.0	150597	3	US-09-949-016-15379	Sequence 15379, A
52	15.4	67.0	767677	3	US-09-949-016-12147	Sequence 12147, A
53	15.4	67.0	767677	3	US-09-949-016-17361	Sequence 17361, A
54	15.2	66.1	25	3	US-09-396-196G-27431	Sequence 27431, A
55	15.2	66.1	372	3	US-09-453-702B-33	Sequence 33, Appl
56	15.2	66.1	372	3	US-10-114-170-33	Sequence 33, Appl
c 57	15.2	66.1	441	3	US-09-252-991A-6220	Sequence 6220, Ap
c 58	15.2	66.1	519	3	US-09-252-991A-7910	Sequence 7910, Ap
59	15.2	66.1	529	3	US-09-533-559-4103	Sequence 4103, Ap

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OM nucleic - nucleic search, using sw model

Run on: July 1, 2006, 04:38:10 ; Search time 320.184 Seconds
(without alignments)
882.666 Million cell updates/sec

Title: US-10-630-536-6

Perfect score: 23

Sequence: 1 cgtcgatgactttctgacggcac 23

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

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	1	23	100.0	23	11	US-10-630-536-6	Sequence 6, Appli
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	3	17.8	77.4	1443	8	US-10-282-122A-29096	Sequence 29096, A
	4	17.8	77.4	1443	10	US-10-467-657-4395	Sequence 4395, Ap
c	5	17.2	74.8	25	9	US-10-719-900-710490	Sequence 710490,
	6	17.2	74.8	738	3	US-09-974-300-5019	Sequence 5019, Ap
	7	17.2	74.8	1974	8	US-10-282-122A-28853	Sequence 28853, A
	8	17.2	74.8	1974	10	US-10-467-657-4781	Sequence 4781, Ap
	9	17.2	74.8	1977	8	US-10-282-122A-29788	Sequence 29788, A
c	10	17.2	74.8	48275	10	US-10-915-740A-48	Sequence 48, Appli
c	11	17.2	74.8	56390	13	US-11-097-143-31168	Sequence 31168, A
	12	17.2	74.8	2242716	10	US-10-915-740A-1068	Sequence 1068, Ap
	13	16.8	73.0	25	11	US-10-933-982-188166	Sequence 188166,
c	14	16.8	73.0	727	8	US-10-424-599-74159	Sequence 74159, A
	15	16.8	73.0	2256646	8	US-10-470-565-1	Sequence 1, Appli
c	16	16.6	72.2	25	6	US-10-098-263B-105751	Sequence 105751,
c	17	16.6	72.2	363	9	US-10-357-930-6364	Sequence 6364, Ap
c	18	16.6	72.2	465	10	US-10-450-763-14970	Sequence 14970, A
c	19	16.6	72.2	513	3	US-09-738-626-96	Sequence 96, Appli
	20	16.6	72.2	543	4	US-09-925-065A-883416	Sequence 883416,
	21	16.6	72.2	543	5	US-09-925-065A-883416	Sequence 883416,
c	22	16.6	72.2	636	13	US-11-006-098-285	Sequence 285, App
	23	16.6	72.2	834	8	US-10-267-502-115	Sequence 115, App
	24	16.6	72.2	1159	13	US-11-097-143-24674	Sequence 24674, A
c	25	16.6	72.2	1275	9	US-10-755-087-60	Sequence 60, Appli
	26	16.6	72.2	1650	10	US-10-450-763-25171	Sequence 25171, A
c	27	16.6	72.2	1988	8	US-10-425-114-26237	Sequence 26237, A
c	28	16.6	72.2	5275	9	US-10-755-087-59	Sequence 59, Appli
c	29	16.6	72.2	34361	13	US-11-097-143-24673	Sequence 24673, A
	30	16.6	72.2	3309400	3	US-09-738-626-1	Sequence 1, Appli
c	31	16.4	71.3	109	2	US-08-911-824-12	Sequence 12, Appli
c	32	16.4	71.3	642	12	US-10-301-480-347442	Sequence 347442,
c	33	16.4	71.3	642	12	US-10-301-480-960851	Sequence 960851,
c	34	16.4	71.3	643	4	US-09-925-065A-269906	Sequence 269906,
c	35	16.4	71.3	643	5	US-09-925-065A-269906	Sequence 269906,
c	36	16.4	71.3	1125	2	US-08-911-824-51	Sequence 51, Appli
	37	16.4	71.3	1696	10	US-10-750-185-58729	Sequence 58729, A
	38	16.4	71.3	1696	10	US-10-750-623-58729	Sequence 58729, A
c	39	16.4	71.3	1860	2	US-08-911-824-53	Sequence 53, Appli
	40	16.4	71.3	7500	8	US-10-468-027-1	Sequence 1, Appli
	41	16.4	71.3	7506	3	US-09-815-379-7	Sequence 7, Appli
	42	16.4	71.3	7506	16	US-11-285-818-7	Sequence 7, Appli
	43	16.2	70.4	263	9	US-10-425-115-120427	Sequence 120427,
c	44	16.2	70.4	546	4	US-09-925-065A-282231	Sequence 282231,
c	45	16.2	70.4	546	4	US-09-925-065A-282232	Sequence 282232,
c	46	16.2	70.4	546	5	US-09-925-065A-282231	Sequence 282231,
c	47	16.2	70.4	546	5	US-09-925-065A-282232	Sequence 282232,
c	48	16.2	70.4	554	12	US-10-301-480-359156	Sequence 359156,
c	49	16.2	70.4	554	12	US-10-301-480-359157	Sequence 359157,
c	50	16.2	70.4	554	12	US-10-301-480-972565	Sequence 972565,
c	51	16.2	70.4	554	12	US-10-301-480-972566	Sequence 972566,
	52	16.2	70.4	559	8	US-10-767-701-316	Sequence 316, App
	53	16.2	70.4	590	3	US-09-925-298-194	Sequence 194, App
	54	16.2	70.4	590	6	US-10-102-806-194	Sequence 194, App

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OM nucleic - nucleic search, using sw model

Run on: July 1, 2006, 04:39:12 ; Search time 23.8804 Seconds
(without alignments)
1138.902 Million cell updates/sec

Title: US-10-630-536-6

Perfect score: 23

Sequence: 1 cgtcgatgactttctgacggcac 23

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 809770 seqs, 591248006 residues

Total number of hits satisfying chosen parameters: 1619540

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

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3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq:
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*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Query Score	Match	Length	DB	ID	Description
c 1	17.4	75.7	1432	6	US-10-449-902-9967	Sequence 9967, Ap

c	2	16.6	72.2	30	6	US-10-548-484-47	Sequence 47, Appl
c	3	16.4	71.3	1000	7	US-11-266-748A-197438	Sequence 197438,
c	4	16.2	70.4	599	7	US-11-266-748A-13758	Sequence 13758, A
c	5	16.2	70.4	599	7	US-11-266-748A-176891	Sequence 176891,
c	6	16.2	70.4	599	7	US-11-266-748A-249917	Sequence 249917,
c	7	16.2	70.4	599	7	US-11-266-748A-310434	Sequence 310434,
c	8	16.2	70.4	623	7	US-11-266-748A-82480	Sequence 82480, A
c	9	16.2	70.4	623	7	US-11-266-748A-135291	Sequence 135291,
c	10	16.2	70.4	750	7	US-11-266-748A-286458	Sequence 286458,
c	11	16.2	70.4	750	7	US-11-266-748A-337887	Sequence 337887,
c	12	16.2	70.4	750	7	US-11-266-748A-396917	Sequence 396917,
c	13	16.2	70.4	750	7	US-11-266-748A-467963	Sequence 467963,
c	14	16.2	70.4	1968	7	US-11-217-529-1728	Sequence 1728, Ap
c	15	16.2	70.4	5642	7	US-11-266-748A-28401	Sequence 28401, A
c	16	15.8	68.7	139515	7	US-11-266-748A-59425	Sequence 59425, A
c	17	15.6	67.8	863	6	US-10-449-902-7490	Sequence 7490, Ap
c	18	15.6	67.8	1118	7	US-11-266-748A-171217	Sequence 171217,
c	19	15.6	67.8	1406	6	US-10-449-902-3044	Sequence 3044, Ap
c	20	15.6	67.8	1933	6	US-10-449-902-14182	Sequence 14182, A
c	21	15.6	67.8	1940	6	US-10-449-902-24465	Sequence 24465, A
c	22	15.6	67.8	2534	6	US-10-449-902-20488	Sequence 20488, A
c	23	15.6	67.8	4018	6	US-10-449-902-15709	Sequence 15709, A
c	24	15.4	67.0	664	7	US-11-266-748A-16575	Sequence 16575, A
c	25	15.4	67.0	780	7	US-11-266-748A-51263	Sequence 51263, A
c	26	15.4	67.0	839	7	US-11-266-748A-53185	Sequence 53185, A
c	27	15.4	67.0	911	7	US-11-266-748A-164942	Sequence 164942,
c	28	15.4	67.0	919	7	US-11-266-748A-5978	Sequence 5978, Ap
c	29	15.4	67.0	1291	7	US-11-266-748A-226775	Sequence 226775,
c	30	15.4	67.0	2378	7	US-11-266-748A-76596	Sequence 76596, A
c	31	15.4	67.0	2378	7	US-11-266-748A-129407	Sequence 129407,
c	32	15.2	66.1	25	7	US-11-217-529-157618	Sequence 157618,
c	33	15.2	66.1	383	7	US-11-266-748A-419015	Sequence 419015,
c	34	15.2	66.1	440	6	US-10-953-349-5917	Sequence 5917, Ap
c	35	15.2	66.1	480	7	US-11-266-748A-231028	Sequence 231028,
c	36	15.2	66.1	690	7	US-11-217-529-82027	Sequence 82027, A
c	37	15.2	66.1	822	6	US-10-471-571A-2345	Sequence 2345, Ap
c	38	15.2	66.1	977	6	US-10-953-349-38966	Sequence 38966, A
c	39	15.2	66.1	1000	7	US-11-266-748A-195958	Sequence 195958,
c	40	15.2	66.1	1000	7	US-11-266-748A-408223	Sequence 408223,
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c	42	15.2	66.1	1029	6	US-10-449-902-4545	Sequence 4545, Ap
c	43	15.2	66.1	1252	6	US-10-449-902-15361	Sequence 15361, A
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c	46	15.2	66.1	1430	6	US-10-449-902-28031	Sequence 28031, A
c	47	15.2	66.1	2067	7	US-11-217-529-1780	Sequence 1780, Ap
c	48	15.2	66.1	2370	7	US-11-217-529-3430	Sequence 3430, Ap
c	49	15.2	66.1	2721	6	US-10-449-902-25970	Sequence 25970, A
c	50	15.2	66.1	3219	7	US-11-217-529-79	Sequence 79, Appl
c	51	15.2	66.1	3544	7	US-11-266-748A-60407	Sequence 60407, A
c	52	15.2	66.1	3653	7	US-11-266-748A-23838	Sequence 23838, A
c	53	15.2	66.1	162354	7	US-11-266-748A-23437	Sequence 23437, A
c	54	15	65.2	501	7	US-11-266-748A-373946	Sequence 373946,
c	55	15	65.2	501	7	US-11-266-748A-457325	Sequence 457325,
c	56	15	65.2	667	6	US-10-953-349-29188	Sequence 29188, A
c	57	15	65.2	781	6	US-10-449-902-7495	Sequence 7495, Ap
c	58	15	65.2	1113	7	US-11-217-529-2143	Sequence 2143, Ap
c	59	15	65.2	1200	6	US-10-513-951-1	Sequence 1, Appl
c	60	15	65.2	1263	6	US-10-953-349-24782	Sequence 24782, A
c	61	15	65.2	1342	6	US-10-449-902-13269	Sequence 13269, A
c	62	15	65.2	1351	6	US-10-449-902-15822	Sequence 15822, A

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OM nucleic - nucleic search, using sw model

Run on: July 1, 2006, 04:17:07 ; Search time 834.328 Seconds
(without alignments)
1541.534 Million cell updates/sec

Title: US-10-630-536-6

Perfect score: 23

Sequence: 1 cgtcgatgactttctgacggcac 23

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : EST:*

1: gb_est1:*

2: gb_est3:*

3: gb_est4:*

4: gb_est5:*

5: gb_est6:*

6: gb_htc:*

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10: gb_est9:*

11: gb_gss1:*

12: gb_gss2:*

13: gb_gss3:*

14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Query					Description
		Score	Match	Length	DB	ID	
c	1	18.8	81.7	843	2	BI552452	BI552452 603196152
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	4	18.2	79.1	659	8	CV749968	CV749968 SJL2-006
c	5	18.2	79.1	683	3	BM595095	BM595095 170006874
c	6	18.2	79.1	763	4	BX606660	BX606660 BX606660
c	7	18.2	79.1	806	13	CL740054	CL740054 OR_BBa007
	8	18.2	79.1	924	8	CV455016	CV455016 EST908925
	9	18	78.3	667	10	DT123661	DT123661 JGI_ANNO8
	10	17.8	77.4	516	13	CZ677176	CZ677176 OM_Ba023
c	11	17.8	77.4	525	13	CZ058768	CZ058768 OM_Ba005
	12	17.8	77.4	597	11	AQ991590	AQ991590 Rfc02585
	13	17.8	77.4	658	3	BQ414930	BQ414930 GA_Ed009
c	14	17.8	77.4	669	9	DN382728	DN382728 LIB38534
	15	17.8	77.4	672	3	BQ415082	BQ415082 GA_Ed009
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	18	17.8	77.4	826	10	DT466964	DT466964 GH_CHX19K
	19	17.8	77.4	869	14	AG839434	AG839434 Oryza sat
	20	17.6	76.5	1012	4	BX398870	BX398870 BX398870
	21	17.4	75.7	774	12	CG178031	CG178031 PUIMG92TB
	22	17.4	75.7	862	12	CG145737	CG145737 PUIFI37TD
c	23	17.2	74.8	234	5	CK744115	CK744115 ltu01-17m
	24	17.2	74.8	398	9	CX619746	CX619746 GABR1_47
c	25	17.2	74.8	507	2	BI377699	BI377699 BFLG3_001
	26	17.2	74.8	532	10	DW567646	DW567646 EST_ss1
	27	17.2	74.8	542	10	DT710673	DT710673 s13dFA40E
c	28	17.2	74.8	573	2	BI380338	BI380338 BFLG1_001
	29	17.2	74.8	583	10	DT710719	DT710719 s13dFA39B
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c	31	17.2	74.8	624	5	CF396743	CF396743 RTDS2_24
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c	37	17.2	74.8	744	10	DT806162	DT806162 Hh_emG_06
c	38	17.2	74.8	776	14	AG053067	AG053067 Pan_trogl
	39	17.2	74.8	795	5	CK177973	CK177973 EST767293
c	40	17.2	74.8	797	12	BZ975468	BZ975468 PUFJU69TD
c	41	17.2	74.8	829	5	CK177972	CK177972 EST767292
	42	17.2	74.8	836	14	DU870542	DU870542 98858 Tom
c	43	17.2	74.8	859	14	CR245554	CR245554 Forward s
c	44	17.2	74.8	870	8	CN168957	CN168957 AGENCOURT
c	45	17.2	74.8	905	11	BH401834	BH401834 AG-ND-149
c	46	17.2	74.8	930	7	BE270919	BE270919 600943796
	47	17.2	74.8	953	3	BQ070370	BQ070370 AGENCOURT
	48	17.2	74.8	968	14	DU859776	DU859776 65066 Tom
	49	17.2	74.8	1021	4	BX339220	BX339220 BX339220
	50	17.2	74.8	1365	14	AJ858811	AJ858811 Brassica
	51	17.2	74.8	1593	7	BF664382	BF664382 602146044
c	52	17.2	74.8	1998	6	CNS0AE01	BX815525 Arabidops
	53	17	73.9	560	9	DB277756	DB277756 DB277756

SCORE Search Results Details for Application 10

630-536-7.rge

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This page gives you Search Results detail for the Application 10630536 and Search Result us-10-6:
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OM nucleic - nucleic search, using sw model

Run on: July 1, 2006, 03:55:42 ; Search time 491.763 Seconds
 (without alignments)
 4291.222 Million cell updates/sec

Title: US-10-630-536-7
 Perfect score: 33
 Sequence: 1 cgagatagccctgataaacgcttcacagttatggc 33

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 150 summaries

Database : GenEmbl:
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 2: gb_pat:
 3: gb_ph:
 4: gb_pl:
 5: gb_pr:
 6: gb_ro:
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 8: gb_sy:
 9: gb_un:
 10: gb_vi:
 11: gb_ov:
 12: gb_htg:
 13: gb_in:
 14: gb_om:
 15: gb_ba:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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		Score	Match	Length	DB	ID	
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	2	33	100.0	147	2	CS001827	CS001827 Sequence
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	4	33	100.0	100984	15	AF053947	AF053947 Yersinia
c	5	33	100.0	100990	2	AR487637	AR487637 Sequence
c	6	33	100.0	100990	15	AF074611	AF074611 Yersinia
	7	33	100.0	106642	15	AE017045	AE017045 Yersinia
	8	33	100.0	137036	15	AJ698720	AJ698720 Yersinia
	9	31.4	95.2	106516	15	STYPPHCM2	AL513384 Salmonell
	10	22.6	68.5	1263	13	AK174551	AK174551 Ciona int
	11	21.4	64.8	125258	12	AC141201	AC141201 Rattus no
c	12	21.4	64.8	255875	12	AC111893	AC111893 Rattus no
c	13	21.4	64.8	290386	12	AC094511	AC094511 Rattus no
	14	21	63.6	165299	6	AC162280	AC162280 Mus muscu
	15	21	63.6	180155	6	AC112273	AC112273 Mus muscu
c	16	20.8	63.0	106763	5	AP002091	AP002091 Homo sapi
	17	20.8	63.0	110000	12	CT005253_5	Continuation (6 of
c	18	20.8	63.0	110000	15	AE014299_19	Continuation (20 o
c	19	20.8	63.0	156754	12	CT573107	CT573107 Danio rer
	20	20.8	63.0	165716	11	CR376858	CR376858 Zebrafish
	21	20.8	63.0	169358	12	CR318602	CR318602 Danio rer
	22	20.8	63.0	178927	6	AC165950	AC165950 Mus muscu
	23	20.8	63.0	178942	6	AC154830	AC154830 Mus muscu
c	24	20.8	63.0	180406	11	BX548247	BX548247 Zebrafish
c	25	20.8	63.0	182736	11	BX511146	BX511146 Zebrafish
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c	27	20.6	62.4	54656	12	AC120611	AC120611 Rattus no
	28	20.6	62.4	170059	12	AC150005	AC150005 Mus muscu
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	30	20.6	62.4	198992	12	AC147548	AC147548 Mus muscu
c	31	20.6	62.4	200131	6	AC146977	AC146977 Mus muscu
	32	20.6	62.4	227939	12	AC106610	AC106610 Rattus no
c	33	20.6	62.4	228833	12	CT030172	CT030172 Mus muscu
	34	20.6	62.4	231853	6	AC159290	AC159290 Mus muscu
	35	20.6	62.4	242195	12	AC126644	AC126644 Rattus no
	36	20.6	62.4	327712	12	CT030171	CT030171 Mus muscu
	37	20.4	61.8	110000	4	CR382138_06	Continuation (7 of
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	39	20.2	61.2	1603	10	AF185964	AF185964 Pterostyl
	40	20.2	61.2	1680	10	AB079647	AB079647 Ornithoga
	41	20.2	61.2	4196	15	AF049633	AF049633 Helicobac
c	42	20.2	61.2	110000	4	AP007175_12	Continuation (13 o
	43	20.2	61.2	110000	15	AE017180_12	Continuation (13 o
	44	20.2	61.2	118227	12	AC148516	AC148516 Canis fam
c	45	20.2	61.2	162685	6	AC110880	AC110880 Mus muscu
c	46	20.2	61.2	183814	12	AC130955	AC130955 Rattus no
	47	20.2	61.2	222763	12	AC098207	AC098207 Rattus no
c	48	20.2	61.2	222986	12	AC114188	AC114188 Rattus no
	49	20.2	61.2	226532	12	AC110662	AC110662 Rattus no
	50	20.2	61.2	275877	12	AC112118	AC112118 Rattus no
c	51	20	60.6	100000	5	AP000070	AP000070 Homo sapi
	52	20	60.6	143644	12	AC149903	AC149903 Strongylo
c	53	20	60.6	147890	11	CR628334	CR628334 Zebrafish
c	54	20	60.6	150880	12	AC062038	AC062038 Homo sapi
	55	20	60.6	156583	5	AP006304	AP006304 Homo sapi
c	56	20	60.6	166980	12	AC152428	AC152428 Bos tauru

57	20	60.6	181788	12	CR396589	CR396589 Danio rer
58	20	60.6	206809	5	AC004470	AC004470 Homo sapi
59	20	60.6	211750	5	AP006306	AP006306 Homo sapi
c 60	20	60.6	218548	5	AL158035	AL158035 Human DNA
c 61	20	60.6	219711	12	AC126913	AC126913 Rattus no
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66	19.8	60.0	110000	4	AP008208_226	Continuation (227
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c 81	19.6	59.4	2204	6	MMPG119	X13052 Murine cyto
82	19.6	59.4	3437	2	AX097850	AX097850 Sequence
c 83	19.6	59.4	4532	6	AY591672	AY591672 Mus muscu
c 84	19.6	59.4	44426	12	AC101052	AC101052 Mus muscu
c 85	19.6	59.4	65031	12	AC114338	AC114338 Mus muscu
c 86	19.6	59.4	68325	12	AC125250	AC125250 Mus muscu
c 87	19.6	59.4	90400	6	AC165106	AC165106 Mus muscu
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93	19.6	59.4	160144	6	AC160532	AC160532 Mus muscu
c 94	19.6	59.4	162787	6	AC140350	AC140350 Mus muscu
c 95	19.6	59.4	167073	6	AC140351	AC140351 Mus muscu
96	19.6	59.4	167751	6	AC155844	AC155844 Mus muscu
c 97	19.6	59.4	171925	12	AC163952	AC163952 Oryctolag
c 98	19.6	59.4	172117	6	AC115040	AC115040 Mus muscu
c 99	19.6	59.4	172217	6	AC103941	AC103941 Mus muscu
c 100	19.6	59.4	173277	12	AC171314	AC171314 Mus muscu
101	19.6	59.4	186564	6	AC119816	AC119816 Mus muscu
c 102	19.6	59.4	189169	6	AC122548	AC122548 Mus muscu
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c 104	19.6	59.4	190906	6	AL928578	AL928578 Mouse DNA
c 105	19.6	59.4	194163	6	AC108858	AC108858 Mus muscu
106	19.6	59.4	195290	12	AC105798	AC105798 Rattus no
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108	19.6	59.4	201610	6	AL732430	AL732430 Mouse DNA
c 109	19.6	59.4	201949	6	AC153022	AC153022 Mus muscu
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c 111	19.6	59.4	209211	12	AC084883	AC084883 Mus muscu
c 112	19.6	59.4	210663	12	CR759901	CR759901 Danio rer
c 113	19.6	59.4	216195	6	AC109608	AC109608 Mus muscu
c 114	19.6	59.4	217306	12	CR354548	CR354548 Mus muscu
c 115	19.6	59.4	219434	6	AC152168	AC152168 Mus muscu
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c 117	19.6	59.4	242397	12	AC097187	AC097187 Rattus no

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123	19.4	58.8	330	2	BD053676	BD053676 Sequence
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126	19.4	58.8	683	2	CQ739411	CQ739411 Sequence
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c 150	19.4	58.8	119972	6	AL772269	AL772269 Mouse DNA

ALIGNMENTS

RESULT 1
CS001826

LOCUS CS001826 33 bp DNA linear PAT 01-FEB-2005
DEFINITION Sequence 7 from Patent WO2004106553.
ACCESSION CS001826
VERSION CS001826.1 GI:58424081
KEYWORDS .
SOURCE Yersinia pestis
ORGANISM Yersinia pestis
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Yersinia.
REFERENCE 1
AUTHORS McCready, P.M., Radnedge, L., Andersen, G.L., Ott, L.L., Slezak, T.R.,
Kuczmarski, T.A. and Motin, V.L.
TITLE Nucleotide sequences specific to Yersinia pestis and methods for
the detection of Yersinia pestis
JOURNAL Patent: WO 2004106553-A 7 09-DEC-2004;
The Regents of The University of California (US)
FEATURES Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:632"

SCORE Search Results Details for Application 10630536

Search Result us-10-630-536-7.rng.

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This page gives you Search Results detail for the Application 10630536 and Search Result us-10-630-536-7.rng.
[start](#)

[Gc](#)

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: July 1, 2006, 03:53:57 ; Search time 198.947 Seconds
 (without alignments)
 1156.508 Million cell updates/sec

Title: US-10-630-536-7

Perfect score: 33

Sequence: 1 cgagatagccctgataaacgcttcacagtatggc 33

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 150 summaries

Database : N_Geneseq_8:*

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- 2: geneseqn1990s:*
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- 14: geneseqn2005s:*
- 15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query					Description
			Match	Length	DB	ID		
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	2	33	100.0	147	14	ADV04873		Adv04873 Yersinia
c	3	33	100.0	100990	12	ADJ94407		Adj94407 Yersinia
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	5	19.6	59.4	3437	5	AAF92567		Aaf92567 Mouse T2R
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	10	19.4	58.8	6261	4	ABL14623		Ab114623 Drosophil
	11	19.4	58.8	10200	4	ABL14622		Ab114622 Drosophil
c	12	19.4	58.8	149480	6	ABL61947		Ab161947 Colon ade
c	13	19.4	58.8	149480	6	ABL68365		Ab168365 Kidney ca
c	14	19.4	58.8	149480	6	ABL61948		Ab161948 Colon ade
c	15	19.2	58.2	2000	11	ACL37154		Acl37154 Rice stre
	16	19.2	58.2	2200	2	AAQ69009		Aaq69009 2-5A-depe
	17	19.2	58.2	2200	2	AAT03902		Aat03902 Murine pa
	18	19.2	58.2	2200	2	AAT59649		Aat59649 Mouse 2-5
	19	19.2	58.2	2200	2	AAX18505		Aax18505 Mouse 2-5
	20	19.2	58.2	2200	9	ACD27924		Acd27924 Mouse RNA
	21	19.2	58.2	2200	12	ADQ60198		Adq60198 Mouse cDN
	22	19.2	58.2	2422	8	ABZ23872		Abz23872 Mouse OAS
c	23	19.2	58.2	185371	6	ABT10718		Abt10718 Human bre
	24	19	57.6	518	13	ADQ79152		Adq79152 Novel can
c	25	19	57.6	62444	12	ADQ97574		Adq97574 Mouse can
c	26	18.8	57.0	307	6	ABN25754		Abn25754 Human ORF
	27	18.8	57.0	2369	4	ABL17612		Ab117612 Drosophil
c	28	18.6	56.4	1177	5	AAS86722		Aas86722 DNA encod
	29	18.6	56.4	1222	2	AAV69558		Aav69558 Soil deri
	30	18.6	56.4	1674	8	ACA36278		Aca36278 Prokaryot
	31	18.6	56.4	1677	8	ACA19004		Aca19004 Prokaryot
	32	18.6	56.4	2919	6	ABK84676		Abk84676 Human cDN
	33	18.6	56.4	2919	12	ADN03903		Adn03903 Antipsori
	34	18.6	56.4	2919	15	AEF75153		Aef75153 Human pol
	35	18.6	56.4	2921	5	AAS74737		Aas74737 DNA encod
	36	18.6	56.4	3071	2	AT11778		Aat11778 Human chr
	37	18.6	56.4	3470	5	ABV25066		Abv25066 Human pro
	38	18.6	56.4	4502	5	AAS86726		Aas86726 DNA encod
c	39	18.6	56.4	63294	9	ADA02939		Ada02939 Mouse Tle
c	40	18.6	56.4	63294	10	ADB72677		Adb72677 Mouse Tle
c	41	18.6	56.4	63294	12	ADM74534		Adm74534 Murine ca
	42	18.4	55.8	739	4	AAH29378		Aah29378 Drosophil
	43	18.4	55.8	1000	14	AEB85653		Aeb85653 Human pho
	44	18.4	55.8	1216	4	AAL01349		Aal01349 Human rep
	45	18.4	55.8	1216	4	ABL96802		Ab196802 Human tes
	46	18.4	55.8	24515	4	ABL08446		Ab108446 Drosophil
	47	18.4	55.8	25381	4	ABL08082		Ab108082 Drosophil
	48	18.4	55.8	30575	14	AED76254_11		Continuation (12 o
	49	18.4	55.8	110000	6	ABX08336_03		Continuation (4 of
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	52	18.4	55.8	110000	12	ADO50281_03		Continuation (4 of
	53	18.4	55.8	110000	14	AEB85185_03		Continuation (4 of
	54	18.4	55.8	110000	14	AED76254_10		Continuation (11 o
c	55	18.4	55.8	135462	12	ADQ97061		Adq97061 Mouse can
	56	18.2	55.2	219	2	AAQ04709		Aaq04709 SLPIII pr

57	18.2	55.2	219	2	AAT29448	Aat29448 Fibronect
58	18.2	55.2	219	2	AAT84497	Aat84497 FCB-SLPII
59	18.2	55.2	219	2	AAV22189	Aav22189 Nucleotid
60	18.2	55.2	219	3	AAZ88303	Aaz88303 SLPIII ge
61	18.2	55.2	219	4	AAF23378	Aaf23378 FCB-SLP o
62	18.2	55.2	219	4	AAF74342	Aaf74342 Repetitiv
63	18.2	55.2	219	6	ABK99033	Abk99033 Fibronect
64	18.2	55.2	219	10	ADE44981	Ade44981 Recombina
65	18.2	55.2	457	13	ADQ52672	Adq52672 Novel can
66	18.2	55.2	555	13	ADS46996	Ads46996 Bacterial
c 67	18.2	55.2	692	2	ADR02380	Adr02380 A. gossyp
c 68	18.2	55.2	717	2	ADR02073	Adr02073 A. gossyp
c 69	18.2	55.2	772	10	ACF66051	Acf66051 Photorhab
c 70	18.2	55.2	1001	4	AAC88191	Aac88191 Optimum p
c 71	18.2	55.2	1293	13	ADT16929	Adt16929 Plant cDN
72	18.2	55.2	1417	4	AAS59719	Aas59719 Propionib
73	18.2	55.2	1417	8	ACF64648	Acf64648 Propionib
74	18.2	55.2	2797	10	ADC30877	Adc30877 Human nov
75	18.2	55.2	2864	10	ADA53427	Ada53427 Human cod
76	18.2	55.2	3030	4	AAS59658	Aas59658 Propionib
77	18.2	55.2	3030	8	ACF64587	Acf64587 Propionib
78	18.2	55.2	4053	10	ACF68006	Acf68006 Photorhab
79	18.2	55.2	6308	13	ADT05508	Adt05508 Haemophil
80	18.2	55.2	88624	9	AAL62889	Aal62889 Human alp
c 81	18.2	55.2	110000	10	ACF67367_06	Continuation (7 of
c 82	18.2	55.2	110000	10	ACF67367_07	Continuation (8 of
c 83	18.2	55.2	110000	10	ACF65384_0	Acf65384 Photorhab
c 84	18.2	55.2	110000	10	ACF65384_1	Continuation (2 of
c 85	18.2	55.2	173564	13	ABD32953	Abd32953 Human can
86	18	54.5	366	10	ACF67765	Acf67765 Photorhab
87	18	54.5	627	10	ADC93097	Adc93097 E. faeciu
c 88	18	54.5	4870	6	ABQ71017	Abq71017 Listeria
c 89	18	54.5	12026	4	AAK67211	Aak67211 Human imm
90	18	54.5	31926	13	ABD33528	Abd33528 Human can
c 91	18	54.5	39121	11	ACN44168	Acn44168 Mouse gen
92	18	54.5	110000	6	ABA03041_28	Continuation (29 o
c 93	18	54.5	110000	10	ACF65383_3	Continuation (4 of
c 94	18	54.5	110000	10	ACF67367_04	Continuation (5 of
95	18	54.5	110000	14	AED76254_09	Continuation (10 o
96	17.8	53.9	155	6	ABT07970	Abt07970 Human lun
97	17.8	53.9	160	6	ABT07971	Abt07971 Human lun
c 98	17.8	53.9	401	5	ABA13716	Abal3716 Human ner
c 99	17.8	53.9	582	13	ACN46997	Acn46997 Cotton pr
100	17.8	53.9	633	2	AAV24733	Aav24733 H. pylori
101	17.8	53.9	633	2	AAT68008	Aat68008 H. pylori
c 102	17.8	53.9	648	13	ACN53931	Acn53931 Cotton an
103	17.8	53.9	681	13	ADQ48797	Adq48797 Novel can
c 104	17.8	53.9	698	13	ADX35473	Adx35473 Plant ful
c 105	17.8	53.9	726	13	ADX09418	Adx09418 Plant ful
106	17.8	53.9	774	2	AAV24871	Aav24871 H. pylori
107	17.8	53.9	864	2	AAT88157	Aat88157 H. pylori
c 108	17.8	53.9	954	6	ABK74858	Abk74858 Bacillus
c 109	17.8	53.9	1195	13	ADX51605	Adx51605 Plant ful
110	17.8	53.9	1248	6	ABN68911	Abn68911 Streptoco
111	17.8	53.9	1251	14	ADZ38635	Adz38635 Group A S
c 112	17.8	53.9	1349	12	ADO57407	Ado57407 C tetrago
c 113	17.8	53.9	1364	13	ADX12861	Adx12861 Plant ful
114	17.8	53.9	1555	13	ADX09668	Adx09668 Plant ful
c 115	17.8	53.9	1646	13	ADT19108	Adt19108 Plant cDN
116	17.8	53.9	2010	4	ABL09595	Ab109595 Drosophil
117	17.8	53.9	2147	4	ABL09589	Ab109589 Drosophil

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OM nucleic - nucleic search, using sw model

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(without alignments)
1524.607 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c	1	33	100.0	100990	3	US-09-409-800B-2	Sequence 2, Appli
	2	19.6	59.4	3437	5	US-10-770-127-156	Sequence 156, App
	3	19.4	58.8	330	3	US-09-513-999C-34006	Sequence 34006, A
	4	19.4	58.8	1803	3	US-10-104-047-1436	Sequence 1436, Ap
	5	19.2	58.2	2200	2	US-08-462-481-3	Sequence 3, Appli
	6	19.2	58.2	2200	2	US-08-436-771-5	Sequence 5, Appli
	7	19.2	58.2	2200	2	US-08-434-998-5	Sequence 5, Appli
	8	19.2	58.2	2200	2	US-08-487-797-5	Sequence 5, Appli
	9	19.2	58.2	2200	2	US-08-701-005A-3	Sequence 3, Appli
	10	19.2	58.2	2200	2	US-08-479-895-3	Sequence 3, Appli
	11	19.2	58.2	2200	3	US-08-943-956A-3	Sequence 3, Appli
	12	19.2	58.2	2200	3	US-09-393-028-1	Sequence 1, Appli
	13	19.2	58.2	2200	7	PCT-US95-02058-5	Sequence 5, Appli
	14	18.6	56.4	1222	3	US-08-861-774E-83	Sequence 83, Appl
	15	18.6	56.4	2919	3	US-09-949-016-775	Sequence 775, App
	16	18.6	56.4	2920	3	US-09-949-016-4279	Sequence 4279, Ap
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c	18	18.4	55.8	281	3	US-09-270-767-23487	Sequence 23487, A
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	21	18.2	55.2	219	2	US-08-175-155-51	Sequence 51, Appl
	22	18.2	55.2	219	2	US-08-477-509B-86	Sequence 86, Appl
	23	18.2	55.2	219	2	US-08-707-237A-59	Sequence 59, Appl
	24	18.2	55.2	219	3	US-08-482-085B-86	Sequence 86, Appl
	25	18.2	55.2	219	3	US-08-475-411A-34	Sequence 34, Appl
	26	18.2	55.2	219	3	US-08-478-029A-34	Sequence 34, Appl
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c	30	18.2	55.2	601	3	US-09-949-002-5249	Sequence 5249, Ap
c	31	18.2	55.2	692	3	US-08-998-416-1072	Sequence 1072, Ap
c	32	18.2	55.2	717	3	US-08-998-416-765	Sequence 765, App
	33	18.2	55.2	2864	4	US-10-094-749-995	Sequence 995, App
c	34	18.2	55.2	46885	3	US-09-949-016-13848	Sequence 13848, A
	35	18.2	55.2	52174	3	US-09-949-002-573	Sequence 573, App
	36	18.2	55.2	52289	3	US-09-949-002-720	Sequence 720, App
	37	18.2	55.2	77772	3	US-09-949-016-17417	Sequence 17417, A
	38	18.2	55.2	77997	3	US-09-949-016-12249	Sequence 12249, A
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	40	18.2	55.2	177669	3	US-09-949-016-13713	Sequence 13713, A
	41	18	54.5	601	3	US-09-949-016-188290	Sequence 188290,
	42	18	54.5	627	3	US-09-107-532A-2724	Sequence 2724, Ap
	43	18	54.5	158735	3	US-09-949-016-11989	Sequence 11989, A
	44	18	54.5	158735	3	US-09-949-016-17130	Sequence 17130, A
	45	17.8	53.9	155	3	US-10-002-344A-115	Sequence 115, App
	46	17.8	53.9	160	3	US-10-002-344A-116	Sequence 116, App
	47	17.8	53.9	601	3	US-09-949-016-79250	Sequence 79250, A
	48	17.8	53.9	601	3	US-09-949-016-79251	Sequence 79251, A
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c	55	17.6	53.3	505	3	US-09-227-357-73	Sequence 73, Appl
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	57	17.6	53.3	1050	3	US-09-252-991A-10218	Sequence 10218, A
c	58	17.6	53.3	1122	3	US-09-252-991A-9836	Sequence 9836, Ap
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c	60	17.6	53.3	16407	3	US-09-949-016-13226	Sequence 13226, A

61	17.6	53.3	100928	3	US-09-949-016-16926	Sequence 16926, A
c 62	17.6	53.3	118067	3	US-09-497-855A-32	Sequence 32, Appl
c 63	17.6	53.3	312957	3	US-09-949-001-31	Sequence 31, Appl
c 64	17.6	53.3	312972	3	US-09-949-001-34	Sequence 34, Appl
65	17.6	53.3	1830121	3	US-09-557-884-1	Sequence 1, Appl
66	17.6	53.3	1830121	3	US-09-643-990A-1	Sequence 1, Appl
67	17.6	53.3	1830121	3	US-10-158-865-1	Sequence 1, Appl
68	17.4	52.7	253	3	US-09-513-999C-13341	Sequence 13341, A
c 69	17.4	52.7	601	3	US-09-949-016-87170	Sequence 87170, A
c 70	17.4	52.7	601	3	US-09-949-016-87171	Sequence 87171, A
71	17.4	52.7	1247	3	US-09-270-767-1351	Sequence 1351, Ap
72	17.4	52.7	1247	3	US-09-270-767-16633	Sequence 16633, A
73	17.4	52.7	3742	3	US-09-762-194-7	Sequence 7, Appli
c 74	17.4	52.7	3957	3	US-09-976-594-1005	Sequence 1005, Ap
c 75	17.4	52.7	4610	3	US-09-417-822-4	Sequence 4, Appli
c 76	17.4	52.7	4610	3	US-09-957-837A-4	Sequence 4, Appli
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c 78	17.4	52.7	4651	3	US-09-417-822-5	Sequence 5, Appli
c 79	17.4	52.7	4651	3	US-09-957-837A-3	Sequence 3, Appli
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c 81	17.4	52.7	8838	3	US-09-417-822-1	Sequence 1, Appli
c 82	17.4	52.7	8838	3	US-09-957-837A-1	Sequence 1, Appli
83	17.4	52.7	21119	3	US-09-453-702B-111	Sequence 111, App
84	17.4	52.7	21119	3	US-10-114-170-111	Sequence 111, App
c 85	17.4	52.7	65966	3	US-09-949-016-17152	Sequence 17152, A
c 86	17.4	52.7	66933	3	US-09-544-398B-11	Sequence 11, Appl
c 87	17.4	52.7	66933	3	US-09-543-771B-11	Sequence 11, Appl
c 88	17.4	52.7	69924	3	US-09-949-016-15367	Sequence 15367, A
c 89	17.4	52.7	72049	3	US-09-544-398B-9	Sequence 9, Appli
c 90	17.4	52.7	72049	3	US-09-543-771B-9	Sequence 9, Appli
c 91	17.4	52.7	95890	3	US-09-949-016-16412	Sequence 16412, A
c 92	17.4	52.7	98302	3	US-09-949-016-16847	Sequence 16847, A
c 93	17.4	52.7	140844	3	US-09-949-016-14199	Sequence 14199, A
94	17.4	52.7	141454	3	US-09-949-016-12055	Sequence 12055, A
95	17.4	52.7	141455	3	US-09-949-016-17190	Sequence 17190, A
c 96	17.4	52.7	197131	3	US-09-949-016-12675	Sequence 12675, A
c 97	17.4	52.7	197132	3	US-09-949-016-17170	Sequence 17170, A
c 98	17.2	52.1	326	3	US-09-270-767-26852	Sequence 26852, A
c 99	17.2	52.1	339	3	US-09-513-999C-28039	Sequence 28039, A
100	17.2	52.1	601	3	US-09-949-016-54768	Sequence 54768, A
c 101	17.2	52.1	696	3	US-09-270-767-11296	Sequence 11296, A
c 102	17.2	52.1	833	3	US-09-188-930-247	Sequence 247, App
c 103	17.2	52.1	833	3	US-09-312-283C-247	Sequence 247, App
c 104	17.2	52.1	849	3	US-09-188-930-29	Sequence 29, Appl
c 105	17.2	52.1	849	3	US-09-312-283C-29	Sequence 29, Appl
106	17.2	52.1	1128	3	US-09-583-110-1176	Sequence 1176, Ap
107	17.2	52.1	1134	3	US-09-107-433-485	Sequence 485, App
108	17.2	52.1	2048	3	US-09-634-238-181	Sequence 181, App
c 109	17.2	52.1	4105	3	US-09-634-238-182	Sequence 182, App
110	17.2	52.1	4761	3	US-09-543-681A-1157	Sequence 1157, Ap
111	17.2	52.1	4784	3	US-09-634-238-24	Sequence 24, Appl
112	17.2	52.1	6412	3	US-08-652-877-17	Sequence 17, Appl
113	17.2	52.1	6412	3	US-08-476-515A-17	Sequence 17, Appl
c 114	17.2	52.1	11340	3	US-08-961-527-147	Sequence 147, App
115	17.2	52.1	14042	3	US-08-652-877-85	Sequence 85, Appl
116	17.2	52.1	14044	3	US-08-652-877-89	Sequence 89, Appl
117	17.2	52.1	14080	3	US-08-652-877-87	Sequence 87, Appl
118	17.2	52.1	14083	3	US-08-476-515A-83	Sequence 83, Appl
119	17.2	52.1	14086	3	US-08-652-877-83	Sequence 83, Appl
120	17.2	52.1	24942	3	US-09-949-016-13318	Sequence 13318, A
c 121	17.2	52.1	34422	3	US-09-949-016-12701	Sequence 12701, A

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Run on: July 1, 2006, 04:38:10 ; Search time 459.395 Seconds
(without alignments)
882.666 Million cell updates/sec

Title: US-10-630-536-7

Perfect score: 33

Sequence: 1 cgagatagccctgataacgcttcacagtatggc 33

Scoring table: IDENTITY_NUC
Gapext 1.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : Published_Applications_NA_Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
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- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
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- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Query					Description
		Score	Match	Length	DB	ID	
	1	33	100.0	33	11	US-10-630-536-7	Sequence 7, Appli
	2	33	100.0	147	11	US-10-630-536-8	Sequence 8, Appli
c	3	19.8	60.0	240	11	US-10-932-182A-81804	Sequence 81804, A
c	4	19.8	60.0	615	10	US-10-487-901-351	Sequence 351, App
	5	19.6	59.4	637	4	US-09-925-065A-516798	Sequence 516798,
	6	19.6	59.4	637	5	US-09-925-065A-516798	Sequence 516798,
	7	19.6	59.4	3437	3	US-09-510-332-156	Sequence 156, App
	8	19.6	59.4	3437	9	US-10-770-127-156	Sequence 156, App
	9	19.6	59.4	3437	10	US-10-962-365-156	Sequence 156, App
	10	19.4	58.8	1803	7	US-10-104-047-1436	Sequence 1436, Ap
	11	19.4	58.8	1803	16	US-11-072-512-1436	Sequence 1436, Ap
	12	19.4	58.8	6261	13	US-11-097-143-19175	Sequence 19175, A
	13	19.4	58.8	10200	13	US-11-097-143-19174	Sequence 19174, A
c	14	19.4	58.8	149480	3	US-09-873-367C-284	Sequence 284, App
c	15	19.4	58.8	149480	3	US-09-873-367C-285	Sequence 285, App
c	16	19.4	58.8	149480	3	US-09-968-007A-232	Sequence 232, App
c	17	19.4	58.8	149480	10	US-10-843-641A-284	Sequence 284, App
c	18	19.4	58.8	149480	10	US-10-843-641A-285	Sequence 285, App
c	19	19.4	58.8	149480	10	US-10-843-641A-6702	Sequence 6702, Ap
	20	19.2	58.2	2200	6	US-10-339-936-1	Sequence 1, Appli
c	21	19.2	58.2	2306	4	US-09-925-065A-706227	Sequence 706227,
c	22	19.2	58.2	2306	5	US-09-925-065A-706227	Sequence 706227,
c	23	19.2	58.2	3347	6	US-10-027-632-116266	Sequence 116266,
c	24	19.2	58.2	3347	7	US-10-027-632-116266	Sequence 116266,
c	25	19.2	58.2	5865	8	US-10-437-963-76215	Sequence 76215, A
c	26	19.2	58.2	6409	8	US-10-437-963-76223	Sequence 76223, A
	27	19	57.6	413	9	US-10-425-115-97917	Sequence 97917, A
c	28	19	57.6	62444	11	US-10-330-773-551	Sequence 551, App
	29	18.8	57.0	237	8	US-10-424-599-84174	Sequence 84174, A
	30	18.8	57.0	484	9	US-10-425-115-98489	Sequence 98489, A
	31	18.8	57.0	507	4	US-09-925-065A-204648	Sequence 204648,
	32	18.8	57.0	507	5	US-09-925-065A-204648	Sequence 204648,
	33	18.8	57.0	519	12	US-10-301-480-292762	Sequence 292762,
	34	18.8	57.0	519	12	US-10-301-480-906171	Sequence 906171,
	35	18.8	57.0	588	4	US-09-925-065A-379079	Sequence 379079,
	36	18.8	57.0	588	5	US-09-925-065A-379079	Sequence 379079,
	37	18.8	57.0	596	12	US-10-301-480-448355	Sequence 448355,
	38	18.8	57.0	596	12	US-10-301-480-1061764	Sequence 1061764,
	39	18.8	57.0	2369	13	US-11-097-143-23659	Sequence 23659, A
	40	18.8	57.0	713059	6	US-10-027-632-174581	Sequence 174581,
	41	18.8	57.0	713059	7	US-10-027-632-174581	Sequence 174581,
	42	18.6	56.4	189	8	US-10-424-599-91422	Sequence 91422, A
c	43	18.6	56.4	840	11	US-10-932-182A-2823	Sequence 2823, Ap
c	44	18.6	56.4	1177	10	US-10-450-763-22526	Sequence 22526, A
	45	18.6	56.4	1222	3	US-09-924-256A-83	Sequence 83, Appl
	46	18.6	56.4	1674	8	US-10-282-122A-24148	Sequence 24148, A
	47	18.6	56.4	1677	8	US-10-282-122A-6874	Sequence 6874, Ap
	48	18.6	56.4	2921	10	US-10-450-763-10541	Sequence 10541, A
	49	18.6	56.4	3470	9	US-10-357-930-25055	Sequence 25055, A
	50	18.6	56.4	4502	10	US-10-450-763-22530	Sequence 22530, A
c	51	18.6	56.4	63294	3	US-09-997-722-205	Sequence 205, App
	52	18.4	55.8	293	4	US-09-925-065A-494611	Sequence 494611,
	53	18.4	55.8	293	5	US-09-925-065A-494611	Sequence 494611,
c	54	18.4	55.8	465	8	US-10-437-963-69314	Sequence 69314, A

c	55	18.4	55.8	545	16	US-11-096-568A-10249	Sequence 10249, A
c	56	18.4	55.8	600	10	US-10-972-079-78000	Sequence 78000, A
c	57	18.4	55.8	600	10	US-10-972-079-78001	Sequence 78001, A
	58	18.4	55.8	637	4	US-09-925-065A-516799	Sequence 516799,
	59	18.4	55.8	637	4	US-09-925-065A-516800	Sequence 516800,
	60	18.4	55.8	637	5	US-09-925-065A-516799	Sequence 516799,
	61	18.4	55.8	637	5	US-09-925-065A-516800	Sequence 516800,
	62	18.4	55.8	1000	10	US-10-868-397-469	Sequence 469, App
	63	18.4	55.8	1216	3	US-09-764-891-1350	Sequence 1350, Ap
	64	18.4	55.8	24515	13	US-11-097-143-9910	Sequence 9910, Ap
	65	18.4	55.8	25381	13	US-11-097-143-9364	Sequence 9364, Ap
c	66	18.4	55.8	135462	11	US-10-330-773-37	Sequence 37, Appl
	67	18.4	55.8	1691139	6	US-10-067-514-1	Sequence 1, Appli
	68	18.4	55.8	1691139	8	US-10-419-723-1	Sequence 1, Appli
	69	18.4	55.8	1691139	8	US-10-255-120-1	Sequence 1, Appli
	70	18.4	55.8	1691140	10	US-10-868-397-1	Sequence 1, Appli
	71	18.4	55.8	1691140	15	US-11-091-018-1	Sequence 1, Appli
c	72	18.2	55.2	201	9	US-10-719-993-19194	Sequence 19194, A
	73	18.2	55.2	201	9	US-10-719-993-29778	Sequence 29778, A
c	74	18.2	55.2	201	9	US-10-741-600-39029	Sequence 39029, A
	75	18.2	55.2	201	9	US-10-741-600-47660	Sequence 47660, A
	76	18.2	55.2	201	10	US-10-995-561-51898	Sequence 51898, A
	77	18.2	55.2	219	6	US-10-096-986-86	Sequence 86, Appl
c	78	18.2	55.2	545	4	US-09-925-065A-443369	Sequence 443369,
c	79	18.2	55.2	545	5	US-09-925-065A-443369	Sequence 443369,
	80	18.2	55.2	555	7	US-10-369-493-25426	Sequence 25426, A
	81	18.2	55.2	555	11	US-10-932-182A-76293	Sequence 76293, A
c	82	18.2	55.2	573	4	US-09-925-065A-333114	Sequence 333114,
c	83	18.2	55.2	573	5	US-09-925-065A-333114	Sequence 333114,
c	84	18.2	55.2	576	12	US-10-301-480-406739	Sequence 406739,
c	85	18.2	55.2	576	12	US-10-301-480-1020148	Sequence 1020148,
	86	18.2	55.2	584	12	US-10-301-480-503807	Sequence 503807,
	87	18.2	55.2	584	12	US-10-301-480-1117216	Sequence 1117216,
c	88	18.2	55.2	596	12	US-10-301-480-372809	Sequence 372809,
c	89	18.2	55.2	596	12	US-10-301-480-986218	Sequence 986218,
	90	18.2	55.2	603	4	US-09-925-065A-295969	Sequence 295969,
	91	18.2	55.2	603	5	US-09-925-065A-295969	Sequence 295969,
	92	18.2	55.2	604	8	US-10-424-599-86062	Sequence 86062, A
	93	18.2	55.2	621	4	US-09-925-065A-684099	Sequence 684099,
	94	18.2	55.2	621	5	US-09-925-065A-684099	Sequence 684099,
c	95	18.2	55.2	737	6	US-10-027-632-169109	Sequence 169109,
c	96	18.2	55.2	737	7	US-10-027-632-169109	Sequence 169109,
	97	18.2	55.2	749	4	US-09-925-065A-946435	Sequence 946435,
	98	18.2	55.2	749	5	US-09-925-065A-946435	Sequence 946435,
c	99	18.2	55.2	989	12	US-10-301-480-601001	Sequence 601001,
c	100	18.2	55.2	989	12	US-10-301-480-1214410	Sequence 1214410,
	101	18.2	55.2	1058	9	US-10-425-115-34097	Sequence 34097, A
c	102	18.2	55.2	1198	16	US-11-096-568A-15963	Sequence 15963, A
c	103	18.2	55.2	1293	9	US-10-739-930-2255	Sequence 2255, Ap
c	104	18.2	55.2	1309	9	US-10-425-115-62646	Sequence 62646, A
c	105	18.2	55.2	1757	9	US-10-425-115-62641	Sequence 62641, A
	106	18.2	55.2	2864	7	US-10-094-749-995	Sequence 995, App
	107	18.2	55.2	6308	10	US-10-795-159-544	Sequence 544, App
	108	18.2	55.2	60486	9	US-10-719-993-6842	Sequence 6842, Ap
	109	18.2	55.2	60486	9	US-10-741-600-17713	Sequence 17713, A
	110	18.2	55.2	60486	10	US-10-995-561-13310	Sequence 13310, A
	111	18.2	55.2	88624	7	US-10-292-081A-1	Sequence 1, Appli
	112	18.2	55.2	88624	8	US-10-608-397-1	Sequence 1, Appli
c	113	18.2	55.2	1980090	9	US-10-719-993-6815	Sequence 6815, Ap
c	114	18.2	55.2	1980090	9	US-10-741-600-17676	Sequence 17676, A
	115	18	54.5	299	8	US-10-424-599-123985	Sequence 123985,

SCORE Search Results Details for Application 10630536 and Search Result us-10-630-536-7.rnpbn.

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OM nucleic - nucleic search, using sw model

Run on: July 1, 2006, 04:39:12 ; Search time 34.2632 Seconds
(without alignments)
1138.902 Million cell updates/sec

Title: US-10-630-536-7
Perfect score: 33
Sequence: 1 cgagatagccctgataacgcttcacagtatggc 33

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 809770 seqs, 591248006 residues

Total number of hits satisfying chosen parameters: 1619540

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : Published_Applications_NA_New:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query

No.	Score	Match	Length	DB	ID	Description
c 1	19.8	60.0	240	7	US-11-217-529-81804	Sequence 81804, A
c 2	19.2	58.2	2512	6	US-10-449-902-9051	Sequence 9051, Ap
3	18.6	56.4	809	7	US-11-266-748A-219140	Sequence 219140,
c 4	18.6	56.4	840	7	US-11-217-529-2823	Sequence 2823, Ap
5	18.6	56.4	1192	7	US-11-266-748A-251158	Sequence 251158,
c 6	18.6	56.4	1192	7	US-11-266-748A-311675	Sequence 311675,
7	18.6	56.4	2919	7	US-11-266-748A-29636	Sequence 29636, A
8	18.6	56.4	2919	7	US-11-266-748A-32190	Sequence 32190, A
9	18.4	55.8	449	7	US-11-266-748A-168316	Sequence 168316,
c 10	18.4	55.8	545	6	US-10-953-349-26282	Sequence 26282, A
11	18.4	55.8	847	7	US-11-266-748A-367452	Sequence 367452,
c 12	18.4	55.8	847	7	US-11-266-748A-450831	Sequence 450831,
c 13	18.4	55.8	938	7	US-11-266-748A-181866	Sequence 181866,
c 14	18.4	55.8	938	7	US-11-266-748A-194728	Sequence 194728,
15	18.4	55.8	938	7	US-11-266-748A-242406	Sequence 242406,
16	18.2	55.2	553	7	US-11-266-748A-409393	Sequence 409393,
17	18.2	55.2	555	7	US-11-217-529-76293	Sequence 76293, A
c 18	17.8	53.9	405	7	US-11-266-748A-371708	Sequence 371708,
19	17.8	53.9	405	7	US-11-266-748A-455087	Sequence 455087,
c 20	17.8	53.9	427	7	US-11-266-748A-429272	Sequence 429272,
21	17.8	53.9	549	7	US-11-266-748A-423145	Sequence 423145,
c 22	17.8	53.9	879	7	US-11-216-545-1162	Sequence 1162, Ap
23	17.8	53.9	888	7	US-11-266-748A-416585	Sequence 416585,
c 24	17.8	53.9	1645	7	US-11-216-545-933	Sequence 933, App
25	17.8	53.9	261789	7	US-11-260-842-1	Sequence 1, Appli
26	17.6	53.3	310	7	US-11-266-748A-269400	Sequence 269400,
c 27	17.6	53.3	310	7	US-11-266-748A-329917	Sequence 329917,
c 28	17.6	53.3	829	6	US-10-953-349-37645	Sequence 37645, A
29	17.6	53.3	1228	6	US-10-449-902-15791	Sequence 15791, A
c 30	17.6	53.3	1481	7	US-11-216-545-7597	Sequence 7597, Ap
31	17.6	53.3	1722	7	US-11-266-748A-352821	Sequence 352821,
32	17.6	53.3	1722	7	US-11-266-748A-384251	Sequence 384251,
c 33	17.6	53.3	1722	7	US-11-266-748A-436200	Sequence 436200,
34	17.6	53.3	2251	7	US-11-216-545-6151	Sequence 6151, Ap
35	17.6	53.3	2473	6	US-10-196-749-559	Sequence 559, App
36	17.6	53.3	2488	7	US-11-266-748A-27494	Sequence 27494, A
37	17.6	53.3	2488	7	US-11-266-748A-57615	Sequence 57615, A
38	17.6	53.3	2739	7	US-11-266-748A-56100	Sequence 56100, A
c 39	17.4	52.7	523	6	US-10-488-619-2592	Sequence 2592, Ap
40	17.4	52.7	536	7	US-11-266-748A-228502	Sequence 228502,
41	17.4	52.7	584	7	US-11-266-748A-47316	Sequence 47316, A
42	17.4	52.7	1000	7	US-11-266-748A-284080	Sequence 284080,
c 43	17.4	52.7	1000	7	US-11-266-748A-335509	Sequence 335509,
44	17.4	52.7	1000	7	US-11-266-748A-393947	Sequence 393947,
c 45	17.4	52.7	1000	7	US-11-266-748A-464993	Sequence 464993,
46	17.4	52.7	1371	7	US-11-266-748A-5512	Sequence 5512, Ap
47	17.4	52.7	1438	7	US-11-266-748A-168317	Sequence 168317,
48	17.4	52.7	1829	7	US-11-266-748A-188963	Sequence 188963,
49	17.4	52.7	1829	7	US-11-266-748A-194855	Sequence 194855,
50	17.4	52.7	1903	7	US-11-266-748A-69265	Sequence 69265, A
c 51	17.4	52.7	1903	7	US-11-266-748A-122076	Sequence 122076,
c 52	17.4	52.7	2354	7	US-11-216-545-5954	Sequence 5954, Ap
53	17.4	52.7	755217	7	US-11-266-748A-29045	Sequence 29045, A
c 54	17.2	52.1	282	7	US-11-266-748A-229685	Sequence 229685,
c 55	17.2	52.1	345	7	US-11-266-748A-298659	Sequence 298659,
c 56	17.2	52.1	592	7	US-11-266-748A-53182	Sequence 53182, A
c 57	17.2	52.1	632	7	US-11-266-748A-86987	Sequence 86987, A
58	17.2	52.1	632	7	US-11-266-748A-139798	Sequence 139798,
59	17.2	52.1	647	7	US-11-266-748A-209862	Sequence 209862,

c	60	17.2	52.1	656	7	US-11-266-748A-251398	Sequence 251398,
c	61	17.2	52.1	656	7	US-11-266-748A-275431	Sequence 275431,
	62	17.2	52.1	656	7	US-11-266-748A-311915	Sequence 311915,
	63	17.2	52.1	785	7	US-11-266-748A-115367	Sequence 115367,
c	64	17.2	52.1	785	7	US-11-266-748A-157531	Sequence 157531,
	65	17.2	52.1	785	7	US-11-266-748A-220775	Sequence 220775,
	66	17.2	52.1	785	7	US-11-266-748A-394443	Sequence 394443,
c	67	17.2	52.1	785	7	US-11-266-748A-465489	Sequence 465489,
c	68	17.2	52.1	840	7	US-11-266-748A-80086	Sequence 80086, A
	69	17.2	52.1	840	7	US-11-266-748A-132897	Sequence 132897,
c	70	17.2	52.1	1035	7	US-11-217-529-82312	Sequence 82312, A
c	71	17.2	52.1	2907	7	US-11-217-529-191128	Sequence 191128,
c	72	17.2	52.1	118899	7	US-11-189-279-64	Sequence 64, Appl
	73	17.2	52.1	141540	7	US-11-266-748A-59424	Sequence 59424, A
c	74	17	51.5	336	7	US-11-266-748A-171450	Sequence 171450,
	75	17	51.5	336	7	US-11-266-748A-245337	Sequence 245337,
c	76	17	51.5	456	7	US-11-266-748A-230026	Sequence 230026,
c	77	17	51.5	537	7	US-11-217-529-2917	Sequence 2917, Ap
	78	17	51.5	713	7	US-11-266-748A-40053	Sequence 40053, A
	79	17	51.5	713	7	US-11-266-748A-208821	Sequence 208821,
c	80	17	51.5	791	7	US-11-266-748A-80701	Sequence 80701, A
c	81	17	51.5	791	7	US-11-266-748A-110901	Sequence 110901,
	82	17	51.5	791	7	US-11-266-748A-133512	Sequence 133512,
	83	17	51.5	951	7	US-11-217-529-196	Sequence 196, App
c	84	17	51.5	997	7	US-11-266-748A-187022	Sequence 187022,
c	85	17	51.5	1000	7	US-11-266-748A-205752	Sequence 205752,
	86	17	51.5	1000	7	US-11-266-748A-292985	Sequence 292985,
c	87	17	51.5	1000	7	US-11-266-748A-344414	Sequence 344414,
	88	17	51.5	1000	7	US-11-266-748A-404869	Sequence 404869,
c	89	17	51.5	1000	7	US-11-266-748A-475915	Sequence 475915,
	90	17	51.5	1086	7	US-11-266-748A-188130	Sequence 188130,
c	91	17	51.5	1086	7	US-11-266-748A-242223	Sequence 242223,
	92	17	51.5	1329	7	US-11-266-748A-228253	Sequence 228253,
c	93	17	51.5	1468	7	US-11-266-748A-172640	Sequence 172640,
	94	17	51.5	1553	6	US-10-449-902-2904	Sequence 2904, Ap
	95	17	51.5	1655	6	US-10-449-902-20113	Sequence 20113, A
c	96	17	51.5	1861	7	US-11-216-545-2454	Sequence 2454, Ap
	97	17	51.5	1929	7	US-11-216-545-6501	Sequence 6501, Ap
	98	17	51.5	2468	7	US-11-293-697-1043	Sequence 1043, Ap
	99	17	51.5	2499	7	US-11-266-748A-353643	Sequence 353643,
c	100	17	51.5	2499	7	US-11-266-748A-437022	Sequence 437022,
	101	17	51.5	2528	7	US-11-293-697-849	Sequence 849, App
c	102	17	51.5	2590	7	US-11-266-748A-22925	Sequence 22925, A
	103	17	51.5	2822	6	US-10-449-902-13071	Sequence 13071, A
	104	17	51.5	3597	7	US-11-266-748A-58448	Sequence 58448, A
c	105	17	51.5	3831	7	US-11-266-748A-22964	Sequence 22964, A
c	106	17	51.5	3883	7	US-11-266-748A-56376	Sequence 56376, A
c	107	17	51.5	96217	7	US-11-266-748A-59101	Sequence 59101, A
	108	17	51.5	193488	7	US-11-266-748A-24309	Sequence 24309, A
c	109	16.8	50.9	181	7	US-11-266-748A-428294	Sequence 428294,
c	110	16.8	50.9	246	7	US-11-266-748A-414376	Sequence 414376,
	111	16.8	50.9	265	7	US-11-266-748A-375432	Sequence 375432,
c	112	16.8	50.9	265	7	US-11-266-748A-458811	Sequence 458811,
c	113	16.8	50.9	518	7	US-11-266-748A-172126	Sequence 172126,
	114	16.8	50.9	518	7	US-11-266-748A-245508	Sequence 245508,
c	115	16.8	50.9	783	7	US-11-266-748A-10946	Sequence 10946, A
	116	16.8	50.9	805	7	US-11-266-748A-62494	Sequence 62494, A
c	117	16.8	50.9	805	7	US-11-266-748A-65333	Sequence 65333, A
c	118	16.8	50.9	835	7	US-11-266-748A-264915	Sequence 264915,
	119	16.8	50.9	835	7	US-11-266-748A-325432	Sequence 325432,
	120	16.8	50.9	867	7	US-11-266-748A-98087	Sequence 98087, A

SCORE Search Results Details for Application 10630536 and Search Result us-10-630-536-7.rst.

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OM nucleic - nucleic search, using sw model

Run on: July 1, 2006, 04:17:07 ; Search time 1197.08 Seconds
(without alignments)
1541.534 Million cell updates/sec

Title: US-10-630-536-7

Perfect score: 33

Sequence: 1 cgagatagccctgataaacgcttcacagttatggc 33

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : EST:*

1: gb_est1:*

2: gb_est3:*

3: gb_est4:*

4: gb_est5:*

5: gb_est6:*

6: gb_htc:*

7: gb_est2:*

8: gb_est7:*

9: gb_est8:*

10: gb_est9:*

11: gb_gss1:*

12: gb_gss2:*

13: gb_gss3:*

14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Score	Query Match	Length	DB	ID	Description
	1	23	69.7	762	14	AG406700 AG406700 Mus muscu
c	2	22.6	68.5	731	3	BW407049 BW407049
c	3	22.6	68.5	775	3	BW079729 BW079729
	4	21.4	64.8	867	8	CX014404 io70f11.g
c	5	21	63.6	318	7	AV892330 AV892330
c	6	21	63.6	392	7	AV892476 AV892476
c	7	21	63.6	513	3	BP022696 BP022696
c	8	21	63.6	567	7	AV892305 AV892305
c	9	21	63.6	596	7	AV892386 AV892386
c	10	21	63.6	659	3	BW156906 BW156906
c	11	21	63.6	668	3	BW234446 BW234446
	12	21	63.6	670	2	BJ734845 BJ734845
	13	21	63.6	676	5	CD306405 CD306405 StrPu691.
	14	21	63.6	690	2	BJ705420 BJ705420
	15	21	63.6	694	2	BJ738061 BJ738061
c	16	21	63.6	695	7	AV892923 AV892923
	17	21	63.6	703	2	BJ709530 BJ709530
	18	21	63.6	704	2	BJ527686 BJ527686
	19	21	63.6	721	2	BJ708080 BJ708080
	20	21	63.6	722	2	BJ713261 BJ713261
c	21	21	63.6	725	3	BW377887 BW377887
c	22	21	63.6	728	3	BW084457 BW084457
c	23	21	63.6	728	7	AV892276 AV892276
c	24	21	63.6	728	7	AV892495 AV892495
c	25	21	63.6	738	3	BW082867 BW082867
c	26	21	63.6	738	3	BW102440 BW102440
c	27	21	63.6	752	3	BW111676 BW111676
c	28	21	63.6	776	3	BW421668 BW421668
c	29	21	63.6	783	7	AV850207 AV850207
c	30	21	63.6	807	12	CG309824 CG309824 OG3DO96TH
	31	21	63.6	812	2	BJ715326 BJ715326
c	32	21	63.6	874	12	CG213700 CG213700 OG3AH20TH
	33	21	63.6	933	12	CG309836 CG309836 OG3DO96TV
	34	21	63.6	1007	12	CG213708 CG213708 OG3AH20TV
	35	20.8	63.0	386	14	BX142971 BX142971 Danio rer
	36	20.8	63.0	466	11	AQ245808 AQ245808 HS_2058_A
	37	20.8	63.0	472	7	BF152282 BF152282 uz31c07.y
c	38	20.8	63.0	555	11	AZ379939 AZ379939 1M0135J11
	39	20.8	63.0	616	8	CV788229 CV788229 zaa60f10.
c	40	20.6	62.4	664	13	DU190643 DU190643 109853816
c	41	20.4	61.8	543	4	CA005709 CA005709 HU08P18u
	42	20.4	61.8	572	4	CA007777 CA007777 HU08P18r
	43	20.4	61.8	960	14	DU786754 DU786754 APKH1780.
	44	20.4	61.8	1147	9	DR154160 DR154160 49169271
	45	20.2	61.2	351	2	BM383354 BM383354 UI-R-DM1-
c	46	20.2	61.2	396	10	DR910548 DR910548 USDA-FP_1
c	47	20.2	61.2	520	7	BE566800 BE566800 601339793
c	48	20.2	61.2	584	5	CD334344 CD334344 StrPu536.
	49	20.2	61.2	739	8	CV708636 CV708636 UCRPT01_0
c	50	20.2	61.2	860	14	CR216782 CR216782 Forward_s
	51	20.2	61.2	886	2	BI646005 BI646005 603274987
	52	20.2	61.2	957	5	CF814561 CF814561 EST691943
c	53	20.2	61.2	990	12	CL070841 CL070841 CH216-119

54	20	60.6	237	1	AV292963	AV292963 AV292963
55	20	60.6	516	11	AZ929176	AZ929176 479.dif23
c 56	20	60.6	892	10	DT795860	DT795860 126466490
57	20	60.6	952	5	CF223182	CF223182 AGENCOURT
c 58	20	60.6	1290	10	DT774175	DT774175 107518310
59	19.8	60.0	187	2	BI452378	BI452378 GI09_G04
60	19.8	60.0	420	7	AW862434	AW862434 RC0-CT038
61	19.8	60.0	456	14	DX237573	DX237573 OR_ABa012
62	19.8	60.0	483	4	CD143635	CD143635 MG1-0086T
63	19.8	60.0	572	5	CF210095	CF210095 CAB20005_-
64	19.8	60.0	632	3	BU998355	BU998355 HI10M16r
c 65	19.8	60.0	709	8	CV710829	CV710829 UCRPT01_0
c 66	19.8	60.0	713	9	CX542612	CX542612 UCRPT01_5
67	19.8	60.0	754	14	AG508862	AG508862 Mus muscu
c 68	19.8	60.0	792	5	CK632917	CK632917 AM2-AP001
c 69	19.8	60.0	820	10	DV097575	DV097575 ppa01-71t
c 70	19.8	60.0	835	7	BF626518	BF626518 HVSMa001
71	19.8	60.0	840	2	BM020384	BM020384 603649030
c 72	19.8	60.0	868	5	CD573706	CD573706 UCRPT01_0
73	19.8	60.0	948	4	CB275296	CB275296 6HRm257_6
c 74	19.8	60.0	992	12	CC190253	CC190253 CH261-37J
c 75	19.8	60.0	994	4	BX377561	BX377561 BX377561
76	19.8	60.0	1114	10	DW027961	DW027961 CFW242-F0
77	19.8	60.0	1305	9	DN711146	DN711146 CLJ93-E08
78	19.8	60.0	1331	9	DN715403	DN715403 CNB108-A1
79	19.8	60.0	1407	13	CL647804	CL647804 CH213-150
80	19.8	60.0	1418	9	DN700227	DN700227 CLJ28-D08
81	19.8	60.0	1423	9	DN715129	DN715129 CNB106-E0
c 82	19.6	59.4	342	1	AV693944	AV693944 AV693944
83	19.6	59.4	381	4	BY670926	BY670926 BY670926
84	19.6	59.4	420	11	BH406381	BH406381 RPCI-23-4
85	19.6	59.4	427	7	AW390452	AW390452 RC3-ST018
c 86	19.6	59.4	452	3	BQ825770	BQ825770 1030129H0
87	19.6	59.4	454	3	BQ825771	BQ825771 1030129H0
88	19.6	59.4	488	11	AZ695864	AZ695864 RPCI-23-2
89	19.6	59.4	584	11	AZ096654	AZ096654 RPCI-23-1
90	19.6	59.4	635	11	AZ069345	AZ069345 RPCI-23-4
c 91	19.6	59.4	685	1	AB072941	AB072941 AB072941
92	19.6	59.4	720	11	AZ246522	AZ246522 RPCI-23-9
93	19.6	59.4	721	14	AG330283	AG330283 Mus muscu
94	19.6	59.4	748	14	AG527571	AG527571 Mus muscu
95	19.6	59.4	1047	3	BQ924279	BQ924279 AGENCOURT
c 96	19.6	59.4	3947	6	AK034463	AK034463 Mus muscu
c 97	19.4	58.8	228	7	BB302417	BB302417 BB302417
c 98	19.4	58.8	305	14	CR018870	CR018870 Forward_s
c 99	19.4	58.8	378	2	BJ267217	BJ267217 BJ267217
c 100	19.4	58.8	380	7	BF249925	BF249925 pa88d07.y
c 101	19.4	58.8	401	2	BJ267420	BJ267420 BJ267420
102	19.4	58.8	412	11	AQ030694	AQ030694 HS_2192_A
c 103	19.4	58.8	427	4	BY679318	BY679318 BY679318
c 104	19.4	58.8	489	4	CB893264	CB893264 EST646056
105	19.4	58.8	494	11	AZ074221	AZ074221 RPCI-23-3
c 106	19.4	58.8	497	7	BF250836	BF250836 pb04h11.y
c 107	19.4	58.8	542	7	BE515541	BE515541 WHE0614_E
108	19.4	58.8	542	8	CO529360	CO529360 3530_1_19
109	19.4	58.8	559	9	DA930011	DA930011 DA930011
110	19.4	58.8	574	9	DA046585	DA046585 DA046585
111	19.4	58.8	585	5	CF255276	CF255276 mdvn126_c
112	19.4	58.8	587	11	AZ277774	AZ277774 RPCI-23-1
c 113	19.4	58.8	602	2	BJ270750	BJ270750 BJ270750
c 114	19.4	58.8	623	2	BM138015	BM138015 WHE0479_D

SCORE Search Results Details for Application 10

630-536-8.rge

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This page gives you Search Results detail for the Application 10630536 and Search Result us-10-6:
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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: July 1, 2006, 03:55:42 ; Search time 2190.58 Seconds
 (without alignments)
 4291.222 Million cell updates/sec

Title: US-10-630-536-8

Perfect score: 147

Sequence: 1 atttgtcggaaaggtcgcagt.....ccgtcagaaagtcatcgacg 147

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 150 summaries

Database : GenEmbl:
 1: gb_env:
 2: gb_pat:
 3: gb_ph:
 4: gb_pl:
 5: gb_pr:
 6: gb_ro:
 7: gb_sts:
 8: gb_sy:
 9: gb_un:
 10: gb_vi:
 11: gb_ov:
 12: gb_htg:
 13: gb_in:
 14: gb_om:
 15: gb_ba:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Query					Description
		Score	Match	Length	DB	ID	
	1	147	100.0	147	2	CS001827	CS001827 Sequence
	2	147	100.0	96210	15	YPPMT1	AL117211 Yersinia
	3	147	100.0	100984	15	AF053947	AF053947 Yersinia
c	4	147	100.0	100990	2	AR487637	AR487637 Sequence
c	5	147	100.0	100990	15	AF074611	AF074611 Yersinia
	6	147	100.0	106642	15	AE017045	AE017045 Yersinia
	7	147	100.0	137036	15	AJ698720	AJ698720 Yersinia
	8	142.2	96.7	106516	15	STYPPHCM2	AL513384 Salmonell
c	9	35	23.8	110000	4	CR382130_22	Continuation (23 o
	10	33	22.4	33	2	CS001826	CS001826 Sequence
c	11	32	21.8	110000	15	CR522870_30	Continuation (31 o
c	12	31.8	21.6	87538	5	AL158200	AL158200 Human DNA
	13	31.8	21.6	110000	15	CP000086_02	Continuation (3 of
c	14	31.8	21.6	110000	15	CP000110_22	Continuation (23 o
c	15	31.8	21.6	167498	12	AC156781	AC156781 Rhinoloph
	16	31.8	21.6	168235	12	AC166859	AC166859 Oryctolag
	17	31.8	21.6	180429	12	AC165394	AC165394 Oryctolag
c	18	31.6	21.5	1640	2	I08235	I08235 Sequence 1
c	19	31.6	21.5	1640	2	I08236	I08236 Sequence 2
	20	31.6	21.5	1643	15	INS493STY	M28508 Insertion e
	21	31.6	21.5	10478	15	AE012341	AE012341 Xanthomon
c	22	31.6	21.5	110000	15	CP000050_21	Continuation (22 o
c	23	31.6	21.5	132016	12	AC148128	AC148128 Ornithorh
c	24	31.4	21.4	2364	15	STMSSPP	L76204 Streptomyce
c	25	31	21.1	234117	12	AC130985	AC130985 Rattus no
c	26	30.8	21.0	8507	13	DME010298	AJ010298 Drosophil
c	27	30.8	21.0	65557	12	AC010062	AC010062 Drosophil
c	28	30.8	21.0	110000	15	AE016827_04	Continuation (5 of
c	29	30.8	21.0	123010	12	AC009746	AC009746 Drosophil
	30	30.8	21.0	169021	13	CP000206	CP000206 Drosophil
c	31	30.8	21.0	189893	12	AC013254	AC013254 Drosophil
c	32	30.8	21.0	190289	10	MCU60315	U60315 Molluscum c
c	33	30.8	21.0	201451	12	AC013831	AC013831 Drosophil
c	34	30.6	20.8	913	7	BV467756	BV467756 G591P6008
	35	30.6	20.8	274094	12	AC163465	AC163465 Bos tauru
	36	30.4	20.7	110000	15	CP000090_30	Continuation (31 o
	37	30.4	20.7	150494	6	AC091617	AC091617 Rattus no
c	38	30.4	20.7	167694	12	CT033816	CT033816 Danio rer
c	39	30.4	20.7	169938	12	AC167145	AC167145 Bos tauru
c	40	30.4	20.7	185266	11	BX511261	BX511261 Zebrafish
c	41	30.4	20.7	197473	11	BX247866	BX247866 Zebrafish
c	42	30.4	20.7	241486	12	AC112561	AC112561 Rattus no
c	43	30.4	20.7	269708	12	AC097787	AC097787 Rattus no
c	44	30.4	20.7	289209	12	AC127408	AC127408 Rattus no
c	45	30.2	20.5	13360	15	AE005797	AE005797 Caulobact
c	46	30.2	20.5	72609	4	CR382129_32	Continuation (33 o
c	47	30.2	20.5	110000	4	CR382129_31	Continuation (32 o
	48	30.2	20.5	110000	15	BA000040_08	Continuation (9 of
	49	30.2	20.5	232636	12	CR931783	CR931783 Danio rer
	50	30	20.4	1119	2	AX652911	AX652911 Sequence
	51	30	20.4	1268	4	AY344487	AY344487 Oryza sat
	52	30	20.4	1310	4	AY323488	AY323488 Oryza sat
	53	30	20.4	1955	4	AK101824	AK101824 Oryza sat
	54	30	20.4	7306	12	AC015067	AC015067 Drosophil
	55	30	20.4	100168	4	AP003826	AP003826 Oryza sat
	56	30	20.4	110000	4	AP008213_041	Continuation (42 o

c	57	30	20.4	121474	12	AC007150	AC007150 Drosophil
c	58	30	20.4	153484	12	AC160218	AC160218 Atelerix
	59	30	20.4	156063	12	AC146732	AC146732 Otolemur
	60	30	20.4	156691	11	BX914195	BX914195 Zebrafish
c	61	30	20.4	163162	13	AC006247	AC006247 Drosophil
c	62	30	20.4	164900	12	AC175627	AC175627 Atelerix
c	63	30	20.4	175868	12	AC113565	AC113565 Canis fam
	64	30	20.4	179545	12	AC146737	AC146737 Otolemur
	65	30	20.4	221945	13	AE003819	AE003819 Drosophil
c	66	29.8	20.3	1860	2	AR384175	AR384175 Sequence
c	67	29.8	20.3	7944	15	AB040071	AB040071 Streptomy
	68	29.8	20.3	110000	12	AP006493_0	AP006493 Cyanidios
	69	29.8	20.3	159872	12	CR931724	CR931724 Danio rer
c	70	29.6	20.1	1038	1	AY836625	AY836625 Unculture
c	71	29.6	20.1	1062	2	AR625957	AR625957 Sequence
c	72	29.6	20.1	2454	4	AF022816	AF022816 Chlamydom
	73	29.6	20.1	5467	2	AR619308	AR619308 Sequence
c	74	29.6	20.1	110000	15	CP000151_28	Continuation (29 o
c	75	29.6	20.1	110000	15	AE014184_06	Continuation (7 of
	76	29.6	20.1	173988	12	AC166210	AC166210 Oryctolag
	77	29.6	20.1	187110	6	AC131303	AC131303 Mus muscu
c	78	29.6	20.1	189349	12	AC174410	AC174410 Oryctolag
	79	29.6	20.1	192016	6	AC099582	AC099582 Mus muscu
	80	29.6	20.1	200904	11	CR376854	CR376854 Zebrafish
	81	29.6	20.1	201352	12	AC158610	AC158610 Mus muscu
c	82	29.6	20.1	204128	5	AC150904	AC150904 Pan trogl
c	83	29.6	20.1	214578	6	AC164579	AC164579 Mus muscu
c	84	29.6	20.1	227214	15	BX572608	BX572608 Rhodopseu
c	85	29.6	20.1	250218	6	AC158662	AC158662 Mus muscu
	86	29.6	20.1	277754	12	AC055704	AC055704 Mus muscu
	87	29.6	20.1	324050	15	BX251410	BX251410 Tropheym
	88	29.4	20.0	1247	2	AR496391	AR496391 Sequence
	89	29.4	20.0	1247	2	AR511673	AR511673 Sequence
c	90	29.4	20.0	1335	11	BX935907	BX935907 Gallus ga
	91	29.4	20.0	2478	2	CQ589338	CQ589338 Sequence
	92	29.4	20.0	2640	13	AF238306	AF238306 Drosophil
	93	29.4	20.0	2677	13	AY119616	AY119616 Drosophil
c	94	29.4	20.0	3037	11	BC068920	BC068920 Xenopus 1
	95	29.4	20.0	5264	2	CQ589337	CQ589337 Sequence
c	96	29.4	20.0	72932	12	AC015300	AC015300 Drosophil
c	97	29.4	20.0	132415	12	AC034276	AC034276 Homo sapi
	98	29.4	20.0	153559	12	AC025000	AC025000 Homo sapi
c	99	29.4	20.0	153559	12	AC025000	AC025000 Homo sapi
	100	29.4	20.0	172281	5	AC068492	AC068492 Homo sapi
	101	29.4	20.0	176735	13	AC007810	AC007810 Drosophil
	102	29.4	20.0	178100	13	AC009742	AC009742 Drosophil
	103	29.4	20.0	212941	13	AE003719	AE003719 Drosophil
	104	29.4	20.0	267739	12	AC169595	AC169595 Bos tauru
	105	29.4	20.0	349142	15	BX572599	BX572599 Rhodopseu
	106	29.2	19.9	4206	15	MAU74385	U74385 Methylomicr
c	107	29.2	19.9	53291	12	AC104745	AC104745 Mus muscu
	108	29.2	19.9	73267	13	CP000171	CP000171 Drosophil
c	109	29.2	19.9	93240	12	AC007586	AC007586 Drosophil
	110	29.2	19.9	99277	12	AC010568	AC010568 Drosophil
	111	29.2	19.9	103842	6	AL840633	AL840633 Mouse DNA
	112	29.2	19.9	104091	13	CP000164	CP000164 Drosophil
	113	29.2	19.9	104875	12	CT009605	CT009605 Danio rer
	114	29.2	19.9	110000	13	AE002665_1	Continuation (2 of
	115	29.2	19.9	110000	13	CP000225_5	Continuation (6 of
c	116	29.2	19.9	110000	13	CP000225_6	Continuation (7 of
	117	29.2	19.9	113098	12	AC009458	AC009458 Drosophil

SCORE Search Results Details for Application : Search Result us-10-630-536-8.rn

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This page gives you Search Results detail for the Application 10630536 and Search Result us-10-6:
start

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: July 1, 2006, 03:53:57 ; Search time 886.22 Seconds
(without alignments)
1156.508 Million cell updates/sec

Title: US-10-630-536-8

Perfect score: 147

Sequence: 1 atttgtcggaaaggtcgcagt.....ccgtcagaaagtcatcgacg 147

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : N_Geneseq_8:*

- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
- 5: geneseqn2001bs:*
- 6: geneseqn2002as:*
- 7: geneseqn2002bs:*
- 8: geneseqn2003as:*
- 9: geneseqn2003bs:*
- 10: geneseqn2003cs:*
- 11: geneseqn2003ds:*
- 12: geneseqn2004as:*
- 13: geneseqn2004bs:*
- 14: geneseqn2005s:*
- 15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Query					Description
		Score	Match	Length	DB	ID	
	1	147	100.0	147	14	ADV04873	Adv04873 Yersinia
c	2	147	100.0	100990	12	ADJ94407	Adj94407 Yersinia
	3	33	22.4	33	14	ADV04872	Adv04872 Yersinia
c	4	31.6	21.5	1641	2	AAQ03677	Aaq03677 Transposa
	5	31.6	21.5	3318	2	AAQ68194	Aaq68194 Tn5099-10
	6	30	20.4	1119	8	ADA69458	Ada69458 Rice gene
	7	30	20.4	1119	12	ADJ39162	Adj39162 Plant cDN
c	8	29.8	20.3	1824	8	ACA35875	Aca35875 Prokaryot
c	9	29.8	20.3	1860	11	ACH95109	Ach95109 Klebsiell
c	10	29.6	20.1	1038	13	ADT49322	Adt49322 Pectate 1
c	11	29.6	20.1	1062	14	ACL70895	Acl70895 M. xanthu
	12	29.6	20.1	5467	14	ACL64240	Acl64240 M. xanthu
	13	29.4	20.0	2478	4	ABL13237	Ab113237 Drosophil
	14	29.4	20.0	5264	4	ABL13236	Ab113236 Drosophil
c	15	29	19.7	2413	10	ADE62765	Ade62765 Human gen
	16	28.8	19.6	1275	13	ADO83407	Ado83407 Plant ful
	17	28.8	19.6	1547	12	ADI43237	Adi43237 Plant tra
	18	28.8	19.6	1547	12	ADO62811	Ado62811 Transcrip
c	19	28.6	19.5	126413	11	ACN45068	Acn45068 Mouse gen
	20	28.4	19.3	469	9	ACC73043	Acc73043 Cat flea
	21	28.4	19.3	469	12	ADL09686	Adl09686 Cat flea
	22	28.2	19.2	385	12	ADO03271	Ado03271 Rice orth
	23	28.2	19.2	1278	13	ADT44538	Adt44538 Bacterial
	24	28.2	19.2	1740	14	ACL65980	Acl65980 M. xanthu
	25	28.2	19.2	11620	14	ACL64547	Acl64547 M. xanthu
c	26	28	19.0	4716	14	ACL67316	Acl67316 M. xanthu
	27	28	19.0	23233	14	ACL64721	Acl64721 M. xanthu
c	28	28	19.0	240000	14	ADZ12006	Adz12006 Mouse ste
c	29	27.8	18.9	735	14	ADX55855	Adx55855 Fine chem
c	30	27.8	18.9	1098	13	ADT45872	Adt45872 Bacterial
	31	27.8	18.9	1578	4	AAS54007	Aas54007 Klebsiell
	32	27.8	18.9	4558	2	AAQ43661	Aaq43661 Acetobact
	33	27.6	18.8	909	11	ABD17353	Abd17353 Pseudomon
c	34	27.6	18.8	1221	11	ABD17720	Abd17720 Pseudomon
c	35	27.4	18.6	296	3	AAF09902	Aaf09902 Fusarium
c	36	27.4	18.6	296	13	ADU53943	Adu53943 Fusarium
c	37	27.4	18.6	296	14	ADZ91946	Adz91946 Fusarium
	38	27.4	18.6	324	14	AEB03328	Aeb03328 Mycobacte
	39	27.4	18.6	324	14	AEA79231	Aea79231 Novel M.
c	40	27.4	18.6	906	8	ACA40499	Aca40499 Prokaryot
c	41	27.4	18.6	110000	4	AAI99682_15	Continuation (16 o
c	42	27.4	18.6	110000	4	AAI99683_15	Continuation (16 o
c	43	27.2	18.5	1188	14	ACL68807	Acl68807 M. xanthu
	44	27.2	18.5	2458	2	AAV84801	Aav84801 Nucleotid
	45	27.2	18.5	2458	10	ABT41749	Abt41749 Toxicity
	46	27.2	18.5	2458	13	ADV41663	Adv41663 Rat cardi
c	47	27.2	18.5	30783	14	ACL64795	Acl64795 M. xanthu
	48	27.2	18.5	101241	11	ACN44740	Acn44740 Mouse gen
c	49	27.2	18.5	110000	2	AAV30458_0	Aav30458 Rhizobium
c	50	27.2	18.5	110000	2	AAV30459_0	Aav30459 Rhizobium
c	51	27.2	18.5	110000	4	AAI99682_31	Continuation (32 o
c	52	27.2	18.5	110000	4	AAI99683_30	Continuation (31 o
c	53	27.2	18.5	110000	4	AAI99683_31	Continuation (32 o
	54	27	18.4	437	12	ADP57740	Adp57740 Soybean c
	55	27	18.4	1601	13	ADX27274	Adx27274 Plant ful
c	56	27	18.4	3132	8	ACA45676	Aca45676 Prokaryot

57	27	18.4	10206	8	AAD55182	Aad55182 Megathura
58	27	18.4	10263	8	AAD55184	Aad55184 Megathura
59	27	18.4	10495	8	AAD55185	Aad55185 Megathura
c 60	27	18.4	110000	2	AAV30458_1	Continuation (2 of
c 61	27	18.4	110000	2	AAV30459_1	Continuation (2 of
c 62	26.8	18.2	774	14	AED25843	Aed25843 DNA encod
c 63	26.8	18.2	817	2	AAT86824	Aat86824 Hevea bra
c 64	26.8	18.2	1091	2	AAT36351	Aat36351 Hevea bra
c 65	26.8	18.2	1489	3	AAC77526	Aac77526 Human ORF
66	26.8	18.2	1657	10	ADD48231	Add48231 Rat gene
67	26.8	18.2	3342	4	AAH23102	Aah23102 Osteoarth
68	26.8	18.2	4964	4	AAH18645	Aah18645 Human cDN
c 69	26.6	18.1	507	3	AAA53561	Aaa53561 Human goo
c 70	26.6	18.1	507	4	AAH26475	Aah26475 Adrenal g
c 71	26.6	18.1	507	6	ABX14174	Abx14174 Human Inc
c 72	26.6	18.1	507	12	ADN59110	Adn59110 Human goo
c 73	26.6	18.1	523	12	ADO21137	Ado21137 Human car
74	26.6	18.1	546	3	AAA53562	Aaa53562 Human goo
75	26.6	18.1	546	4	AAH26476	Aah26476 Adrenal g
76	26.6	18.1	546	6	ABX14175	Abx14175 Human Inc
77	26.6	18.1	546	12	ADN59111	Adn59111 Human goo
c 78	26.6	18.1	582	5	AAF28686	Aaf28686 Human pro
c 79	26.6	18.1	585	5	AAH52149	Aah52149 Human AFP
80	26.6	18.1	746	6	ABQ41419	Abq41419 Oligonucl
c 81	26.6	18.1	746	6	ABQ41418	Abq41418 Oligonucl
82	26.6	18.1	810	4	ABA09258	Aba09258 Human sec
83	26.6	18.1	810	4	AAK53139	Aak53139 Human pol
c 84	26.6	18.1	850	3	AAZ52558	Aaz52558 Human sec
85	26.6	18.1	859	4	AAL01017	Aal01017 Human rep
86	26.6	18.1	859	4	ABL96485	Abl96485 Human tes
c 87	26.6	18.1	963	4	AAK52155	Aak52155 Human pol
c 88	26.6	18.1	963	5	AAF28696	Aaf28696 Human pro
c 89	26.6	18.1	1046	3	AAA53558	Aaa53558 Human goo
c 90	26.6	18.1	1046	4	AAH26472	Aah26472 Human goo
c 91	26.6	18.1	1046	6	ABX14171	Abx14171 Human goo
c 92	26.6	18.1	1046	12	ADN59107	Adn59107 Human goo
c 93	26.6	18.1	1047	8	ACA54350	Aca54350 Prokaryot
c 94	26.6	18.1	1049	3	AAA96356	Aaa96356 cDNA enco
c 95	26.6	18.1	1049	6	ABL88231	Ab188231 Human PRO
c 96	26.6	18.1	1049	6	ABL95720	Ab195720 Human ang
c 97	26.6	18.1	1049	8	ACD28848	Acd28848 Human sec
c 98	26.6	18.1	1049	8	ACA06122	Aca06122 cDNA enco
c 99	26.6	18.1	1049	9	ACA67745	Aca67745 cDNA enco
c 100	26.6	18.1	1049	9	ADA76600	Ada76600 Novel hum
c 101	26.6	18.1	1049	9	ACD42307	Acd42307 Human cDN
c 102	26.6	18.1	1049	10	AAD59373	Aad59373 Human PRO
c 103	26.6	18.1	1049	10	AAD59248	Aad59248 Human PRO
c 104	26.6	18.1	1049	10	ADC29831	Adc29831 Novel hum
c 105	26.6	18.1	1049	10	ADD10608	Add10608 Human sec
c 106	26.6	18.1	1049	10	ADD11568	Add11568 Human sec
c 107	26.6	18.1	1049	10	ADD37361	Add37361 Human sec
c 108	26.6	18.1	1049	10	ACA06179	Aca06179 cDNA enco
c 109	26.6	18.1	1049	12	ADE41569	Ade41569 Human sec
c 110	26.6	18.1	1049	12	ADF09274	Adf09274 Human sec
c 111	26.6	18.1	1049	12	ADH43752	Adh43752 Human PRO
c 112	26.6	18.1	1049	12	ADK83097	Adk83097 Human PRO
c 113	26.6	18.1	1049	14	ADW12506	Adw12506 Human PRO
c 114	26.6	18.1	1374	4	ABL25767	Ab125767 Drosophil
c 115	26.6	18.1	2000	11	ACL35782	Acl35782 Rice stre
c 116	26.6	18.1	2000	11	ACL37773	Acl37773 Rice stre
c 117	26.6	18.1	3030	4	AAH42268	Aah42268 Nucleotid

SCORE Search Results Details for Application 10630536 and Search Result us-10-630-536- 8.rni.

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: July 1, 2006, 04:28:37 ; Search time 180.409 Seconds
(without alignments)
1524.607 Million cell updates/sec

Title: US-10-630-536-8

Perfect score: 147

Sequence: 1 atttgcggaaaggtcgcagt.....ccgtcagaaagtcatcgacg 147

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : Issued_Patents_NA:
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7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*

8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*

9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*

10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
	No.	Score	Match	Length	DB	ID
c 1	147	100.0	100990	3	US-09-409-800B-2	Sequence 2, Appli
c 2	29.8	20.3	1860	3	US-09-489-039A-904	Sequence 904, App
c 3	29.6	20.1	1062	3	US-09-902-540-7358	Sequence 7358, Ap
4	29.6	20.1	5467	3	US-09-902-540-703	Sequence 703, App
5	29.4	20.0	1247	3	US-09-270-767-1351	Sequence 1351, Ap
6	29.4	20.0	1247	3	US-09-270-767-16633	Sequence 16633, A
7	28.8	19.6	601	3	US-09-949-016-80937	Sequence 80937, A
8	28.8	19.6	601	3	US-09-949-016-80938	Sequence 80938, A
c 9	28.8	19.6	199471	3	US-09-949-016-14083	Sequence 14083, A
10	28.2	19.2	1740	3	US-09-902-540-2443	Sequence 2443, Ap
11	28.2	19.2	11620	3	US-09-902-540-1010	Sequence 1010, Ap
c 12	28	19.0	4716	3	US-09-902-540-3779	Sequence 3779, Ap
13	28	19.0	23233	3	US-09-902-540-1184	Sequence 1184, Ap
14	27.8	18.9	4558	2	US-08-309-512-2	Sequence 2, Appli
15	27.8	18.9	4558	7	PCT-US92-08756A-2	Sequence 2, Appli
16	27.6	18.8	909	3	US-09-252-991A-15957	Sequence 15957, A
c 17	27.6	18.8	1221	3	US-09-252-991A-16324	Sequence 16324, A
c 18	27.4	18.6	296	3	US-09-533-559-2425	Sequence 2425, Ap
c 19	27.4	18.6	4403765	3	US-09-103-840A-2	Sequence 2, Appli
c 20	27.4	18.6	4411529	3	US-09-103-840A-1	Sequence 1, Appli
c 21	27.2	18.5	1188	3	US-09-902-540-5270	Sequence 5270, Ap
22	27.2	18.5	2458	3	US-09-071-101-5	Sequence 5, Appli
23	27.2	18.5	2458	3	US-09-369-618-6	Sequence 6, Appli
24	27.2	18.5	2458	3	US-09-369-617-6	Sequence 6, Appli
c 25	27.2	18.5	30783	3	US-09-902-540-1258	Sequence 1258, Ap
c 26	27.2	18.5	536165	3	US-09-214-808-1	Sequence 1, Appli
c 27	27	18.4	369	3	US-09-621-976-10521	Sequence 10521, A
c 28	26.8	18.2	1078	3	US-08-981-256A-4	Sequence 4, Appli
c 29	26.6	18.1	507	3	US-09-105-567A-5	Sequence 5, Appli
c 30	26.6	18.1	507	3	US-09-511-720-5	Sequence 5, Appli
c 31	26.6	18.1	507	3	US-09-844-036A-5	Sequence 5, Appli
32	26.6	18.1	546	3	US-09-105-567A-6	Sequence 6, Appli
33	26.6	18.1	546	3	US-09-511-720-6	Sequence 6, Appli
34	26.6	18.1	546	3	US-09-844-036A-6	Sequence 6, Appli
c 35	26.6	18.1	850	3	US-09-311-021-167	Sequence 167, App
c 36	26.6	18.1	1046	3	US-09-105-567A-2	Sequence 2, Appli
c 37	26.6	18.1	1046	3	US-09-511-720-2	Sequence 2, Appli
c 38	26.6	18.1	1046	3	US-09-844-036A-2	Sequence 2, Appli
c 39	26.6	18.1	1049	4	US-10-036-041-75	Sequence 75, Appli
c 40	26.6	18.1	7178	3	US-09-710-262E-2	Sequence 2, Appli
c 41	26.6	18.1	23496	3	US-09-902-540-5645	Sequence 5645, Ap
42	26.6	18.1	51354	3	US-09-902-540-1270	Sequence 1270, Ap
c 43	26.4	18.0	1530	3	US-09-134-000C-2544	Sequence 2544, Ap
44	26.4	18.0	10144	4	US-09-880-107-2168	Sequence 2168, Ap
45	26.2	17.8	885	3	US-09-489-039A-3762	Sequence 3762, Ap
46	26	17.7	11663	2	US-08-446-932-1	Sequence 1, Appli
47	26	17.7	11663	2	US-08-801-263A-1	Sequence 1, Appli
48	26	17.7	11663	2	US-08-801-263A-7	Sequence 7, Appli
49	26	17.7	11663	3	US-09-102-248-1	Sequence 1, Appli
50	26	17.7	11663	3	US-09-102-248-7	Sequence 7, Appli
51	26	17.7	11663	3	US-09-367-764-1	Sequence 1, Appli
52	26	17.7	11663	3	US-09-367-764-7	Sequence 7, Appli
53	26	17.7	11717	2	US-08-801-263A-4	Sequence 4, Appli
54	26	17.7	11717	3	US-09-102-248-4	Sequence 4, Appli
55	26	17.7	11717	3	US-09-367-764-4	Sequence 4, Appli
c 56	26	17.7	246444	3	US-09-949-016-13113	Sequence 13113, A
57	25.8	17.6	123863	3	US-09-949-016-14202	Sequence 14202, A

c	58	25.6	17.4	733	3	US-09-270-767-1287	Sequence 1287, Ap
c	59	25.6	17.4	733	3	US-09-270-767-16569	Sequence 16569, A
	60	25.6	17.4	861	5	US-09-974-300-6106	Sequence 6106, Ap
	61	25.6	17.4	4334	2	US-08-670-707A-38	Sequence 38, Appl
	62	25.6	17.4	4334	3	US-09-037-601-38	Sequence 38, Appl
	63	25.6	17.4	4334	3	US-09-315-179-38	Sequence 38, Appl
	64	25.6	17.4	4334	5	US-10-187-319-38	Sequence 38, Appl
	65	25.6	17.4	4334	5	US-10-131-510A-38	Sequence 38, Appl
	66	25.6	17.4	4404	3	US-09-523-656-37	Sequence 37, Appl
	67	25.6	17.4	6402	2	US-08-670-707A-36	Sequence 36, Appl
	68	25.6	17.4	6402	3	US-09-037-601-36	Sequence 36, Appl
	69	25.6	17.4	6402	3	US-09-315-179-36	Sequence 36, Appl
	70	25.6	17.4	6402	3	US-09-523-656-29	Sequence 29, Appl
	71	25.6	17.4	6402	5	US-10-187-319-36	Sequence 36, Appl
	72	25.6	17.4	6402	5	US-10-131-510A-36	Sequence 36, Appl
	73	25.6	17.4	141248	3	US-09-949-016-12241	Sequence 12241, A
	74	25.4	17.3	399	2	US-08-470-179-170	Sequence 170, App
	75	25.4	17.3	601	3	US-09-949-016-95336	Sequence 95336, A
	76	25.4	17.3	601	3	US-09-949-016-95514	Sequence 95514, A
	77	25.4	17.3	601	3	US-09-949-016-95692	Sequence 95692, A
	78	25.4	17.3	601	3	US-09-949-016-95870	Sequence 95870, A
	79	25.4	17.3	601	3	US-09-949-016-191629	Sequence 191629,
	80	25.4	17.3	601	3	US-09-949-016-191807	Sequence 191807,
	81	25.4	17.3	601	3	US-09-949-016-191985	Sequence 191985,
	82	25.4	17.3	601	3	US-09-949-016-192163	Sequence 192163,
c	83	25.4	17.3	2783	3	US-09-221-017B-901	Sequence 901, App
	84	25.4	17.3	72455	3	US-09-949-016-13793	Sequence 13793, A
	85	25.4	17.3	104475	3	US-09-949-016-12115	Sequence 12115, A
	86	25.4	17.3	111282	3	US-09-754-250-3	Sequence 3, Appli
	87	25.4	17.3	111282	3	US-10-094-989-3	Sequence 3, Appli
	88	25.4	17.3	203475	3	US-09-949-016-14516	Sequence 14516, A
	89	25.4	17.3	203475	3	US-09-949-016-14517	Sequence 14517, A
	90	25.4	17.3	203475	3	US-09-949-016-14518	Sequence 14518, A
	91	25.4	17.3	203475	3	US-09-949-016-14519	Sequence 14519, A
	92	25.4	17.3	203475	3	US-09-949-016-17226	Sequence 17226, A
	93	25.4	17.3	203475	3	US-09-949-016-17227	Sequence 17227, A
	94	25.4	17.3	203475	3	US-09-949-016-17228	Sequence 17228, A
	95	25.4	17.3	203475	3	US-09-949-016-17229	Sequence 17229, A
	96	25.4	17.3	462589	3	US-09-949-016-12900	Sequence 12900, A
	97	25.4	17.3	476044	3	US-09-949-016-12412	Sequence 12412, A
c	98	25.2	17.1	849	3	US-09-252-991A-11100	Sequence 11100, A
	99	25.2	17.1	852	3	US-09-252-991A-10964	Sequence 10964, A
c	100	25.2	17.1	47184	3	US-09-949-016-12647	Sequence 12647, A
c	101	25.2	17.1	47184	3	US-09-949-016-15531	Sequence 15531, A
	102	25.2	17.1	4403765	3	US-09-103-840A-2	Sequence 2, Appli
	103	25.2	17.1	4411529	3	US-09-103-840A-1	Sequence 1, Appli
c	104	25	17.0	395	3	US-09-270-767-30675	Sequence 30675, A
c	105	25	17.0	520	3	US-09-270-767-14496	Sequence 14496, A
c	106	25	17.0	833	4	US-09-880-107-3038	Sequence 3038, Ap
	107	25	17.0	1068	3	US-09-252-991A-5755	Sequence 5755, Ap
c	108	25	17.0	2136	3	US-09-252-991A-5688	Sequence 5688, Ap
	109	25	17.0	2988	3	US-09-252-991A-5726	Sequence 5726, Ap
	110	25	17.0	3501	2	US-08-524-757-5	Sequence 5, Appli
c	111	25	17.0	20795	3	US-09-949-016-17166	Sequence 17166, A
	112	25	17.0	155266	3	US-09-949-016-13870	Sequence 13870, A
c	113	24.8	16.9	307	3	US-09-513-999C-16394	Sequence 16394, A
c	114	24.8	16.9	655	3	US-09-533-559-2087	Sequence 2087, Ap
c	115	24.8	16.9	777	3	US-09-902-540-6756	Sequence 6756, Ap
	116	24.8	16.9	906	3	US-09-107-532A-3422	Sequence 3422, Ap
c	117	24.8	16.9	2382	3	US-09-489-039A-278	Sequence 278, App
c	118	24.8	16.9	3707	3	US-09-902-540-549	Sequence 549, App

SCORE Search Results Details for Application 10630536 and Search Result us-10-630-536-8.rn

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OM nucleic - nucleic search, using sw model

Run on: July 1, 2006, 04:38:10 ; Search time 2046.39 Seconds
(without alignments)
882.666 Million cell updates/sec

Title: US-10-630-536-8
Perfect score: 147
Sequence: 1 atttgtcggaaaggtcgcagt.....ccgtcagaaagtcatcgacg 147

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : Published_Applications_NA_Main:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

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	1	147	100.0	147	11	US-10-630-536-8	Sequence 8, Appli
	2	33	22.4	33	11	US-10-630-536-7	Sequence 7, Appli
c	3	30.2	20.5	1414	10	US-10-750-185-30136	Sequence 30136, A
c	4	30.2	20.5	1414	10	US-10-750-623-30136	Sequence 30136, A
	5	30	20.4	1119	8	US-10-260-238-162	Sequence 162, App
	6	30	20.4	1119	8	US-10-437-963-92405	Sequence 92405, A
c	7	29.8	20.3	1824	8	US-10-282-122A-23745	Sequence 23745, A
	8	29.4	20.0	2478	13	US-11-097-143-17096	Sequence 17096, A
	9	29.4	20.0	5264	13	US-11-097-143-17095	Sequence 17095, A
c	10	29.2	19.9	2596	9	US-10-425-115-95747	Sequence 95747, A
	11	28.8	19.6	606	4	US-09-925-065A-790070	Sequence 790070,
	12	28.8	19.6	606	5	US-09-925-065A-790070	Sequence 790070,
c	13	28.8	19.6	714	6	US-10-027-632-101701	Sequence 101701,
c	14	28.8	19.6	714	7	US-10-027-632-101701	Sequence 101701,
	15	28.8	19.6	1275	8	US-10-425-114-2127	Sequence 2127, Ap
	16	28.8	19.6	1547	8	US-10-374-780A-1700	Sequence 1700, Ap
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c	18	28.8	19.6	2274	4	US-09-925-065A-90102	Sequence 90102, A
c	19	28.8	19.6	2274	4	US-09-925-065A-90103	Sequence 90103, A
c	20	28.8	19.6	2274	5	US-09-925-065A-90102	Sequence 90102, A
c	21	28.8	19.6	2274	5	US-09-925-065A-90103	Sequence 90103, A
c	22	28.8	19.6	2274	12	US-10-301-480-191343	Sequence 191343,
c	23	28.8	19.6	2274	12	US-10-301-480-191344	Sequence 191344,
c	24	28.8	19.6	2274	12	US-10-301-480-804752	Sequence 804752,
c	25	28.8	19.6	2274	12	US-10-301-480-804753	Sequence 804753,
c	26	28.8	19.6	2940917	6	US-10-027-632-174763	Sequence 174763,
c	27	28.8	19.6	2940917	7	US-10-027-632-174763	Sequence 174763,
c	28	28.6	19.5	126413	6	US-10-087-192-1831	Sequence 1831, Ap
	29	28.4	19.3	469	8	US-10-621-901-118	Sequence 118, App
	30	28.2	19.2	385	8	US-10-412-699B-1684	Sequence 1684, Ap
	31	28.2	19.2	1278	7	US-10-369-493-42976	Sequence 42976, A
	32	28	19.0	1518	7	US-10-156-761-5098	Sequence 5098, Ap
c	33	28	19.0	150298	10	US-10-981-277-52	Sequence 52, Appli
c	34	28	19.0	164910	10	US-10-981-277-53	Sequence 53, Appli
c	35	28	19.0	196151	10	US-10-981-277-51	Sequence 51, Appli
c	36	28	19.0	240001	10	US-10-936-273-32	Sequence 32, Appli
	37	28	19.0	9025608	7	US-10-156-761-1	Sequence 1, Appli
c	38	27.8	18.9	572	12	US-10-301-480-378972	Sequence 378972,
c	39	27.8	18.9	572	12	US-10-301-480-992381	Sequence 992381,
c	40	27.8	18.9	578	4	US-09-925-065A-302784	Sequence 302784,
c	41	27.8	18.9	578	5	US-09-925-065A-302784	Sequence 302784,
c	42	27.8	18.9	608	12	US-10-301-480-42286	Sequence 42286, A
c	43	27.8	18.9	608	12	US-10-301-480-655695	Sequence 655695,
c	44	27.8	18.9	634	6	US-10-027-632-180713	Sequence 180713,
c	45	27.8	18.9	634	7	US-10-027-632-180713	Sequence 180713,
c	46	27.8	18.9	1098	7	US-10-369-493-44310	Sequence 44310, A
c	47	27.8	18.9	1342	8	US-10-767-701-11891	Sequence 11891, A
	48	27.8	18.9	1578	3	US-09-815-242-7644	Sequence 7644, Ap
	49	27.6	18.8	2340	9	US-10-425-115-166962	Sequence 166962,
c	50	27.4	18.6	296	9	US-10-653-047-2425	Sequence 2425, Ap
	51	27.4	18.6	324	10	US-10-755-415-100	Sequence 100, App
	52	27.4	18.6	409	9	US-10-425-115-157550	Sequence 157550,
	53	27.4	18.6	808	9	US-10-425-115-21178	Sequence 21178, A
c	54	27.4	18.6	906	8	US-10-282-122A-28369	Sequence 28369, A

c	55	27.4	18.6	1777	16	US-11-096-568A-20653	Sequence 20653, A
	56	27.2	18.5	477	4	US-09-925-065A-541808	Sequence 541808,
	57	27.2	18.5	477	4	US-09-925-065A-541809	Sequence 541809,
	58	27.2	18.5	477	5	US-09-925-065A-541808	Sequence 541808,
	59	27.2	18.5	477	5	US-09-925-065A-541809	Sequence 541809,
c	60	27.2	18.5	597	8	US-10-767-701-7707	Sequence 7707, Ap
	61	27.2	18.5	2458	8	US-10-152-319A-1451	Sequence 1451, Ap
	62	27.2	18.5	2458	16	US-11-036-196-1451	Sequence 1451, Ap
	63	27.2	18.5	101241	6	US-10-087-192-1339	Sequence 1339, Ap
c	64	27.2	18.5	536165	3	US-09-939-964-1	Sequence 1, Appli
	65	27	18.4	437	3	US-09-987-899-809	Sequence 809, App
	66	27	18.4	1601	8	US-10-425-114-10094	Sequence 10094, A
	67	27	18.4	1897	8	US-10-424-599-89297	Sequence 89297, A
c	68	27	18.4	3132	8	US-10-282-122A-33546	Sequence 33546, A
	69	27	18.4	10206	9	US-10-488-824-1	Sequence 1, Appli
c	70	27	18.4	10206	9	US-10-488-824-2	Sequence 2, Appli
	71	27	18.4	10263	9	US-10-488-824-7	Sequence 7, Appli
c	72	27	18.4	10263	9	US-10-488-824-8	Sequence 8, Appli
	73	27	18.4	10495	9	US-10-488-824-10	Sequence 10, Appli
c	74	27	18.4	10495	9	US-10-488-824-11	Sequence 11, Appli
c	75	26.8	18.2	201	9	US-10-741-600-72531	Sequence 72531, A
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	77	26.8	18.2	626	4	US-09-925-065A-885183	Sequence 885183,
	78	26.8	18.2	626	5	US-09-925-065A-885182	Sequence 885182,
	79	26.8	18.2	626	5	US-09-925-065A-885183	Sequence 885183,
	80	26.8	18.2	1386	7	US-10-156-761-3781	Sequence 3781, Ap
c	81	26.8	18.2	2556	7	US-10-156-761-181	Sequence 181, App
	82	26.8	18.2	3342	3	US-09-765-231A-32	Sequence 32, Appli
c	83	26.8	18.2	125560	9	US-10-741-600-18002	Sequence 18002, A
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c	85	26.6	18.1	507	3	US-09-844-036A-5	Sequence 5, Appli
c	86	26.6	18.1	507	8	US-10-688-128-5	Sequence 5, Appli
	87	26.6	18.1	546	3	US-09-844-036A-6	Sequence 6, Appli
	88	26.6	18.1	546	8	US-10-688-128-6	Sequence 6, Appli
c	89	26.6	18.1	746	9	US-10-363-345A-28009	Sequence 28009, A
	90	26.6	18.1	746	9	US-10-363-345A-28010	Sequence 28010, A
c	91	26.6	18.1	746	10	US-10-363-483A-28009	Sequence 28009, A
	92	26.6	18.1	746	10	US-10-363-483A-28010	Sequence 28010, A
	93	26.6	18.1	810	8	US-10-276-774-1034	Sequence 1034, Ap
	94	26.6	18.1	859	3	US-09-764-891-1018	Sequence 1018, Ap
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c	96	26.6	18.1	1046	8	US-10-688-128-2	Sequence 2, Appli
c	97	26.6	18.1	1047	8	US-10-282-122A-42220	Sequence 42220, A
c	98	26.6	18.1	1049	3	US-09-931-836-75	Sequence 75, Appli
c	99	26.6	18.1	1049	6	US-10-036-342-75	Sequence 75, Appli
c	100	26.6	18.1	1049	6	US-10-036-041-75	Sequence 75, Appli
c	101	26.6	18.1	1049	6	US-10-035-855-75	Sequence 75, Appli
c	102	26.6	18.1	1049	6	US-10-036-214-75	Sequence 75, Appli
c	103	26.6	18.1	1049	6	US-10-035-719-75	Sequence 75, Appli
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c	107	26.6	18.1	1049	6	US-10-036-063-75	Sequence 75, Appli
c	108	26.6	18.1	1049	6	US-10-223-085-319	Sequence 319, App
c	109	26.6	18.1	1049	6	US-10-223-084-319	Sequence 319, App
c	110	26.6	18.1	1049	6	US-10-223-088-319	Sequence 319, App
c	111	26.6	18.1	1049	6	US-10-223-090-319	Sequence 319, App
c	112	26.6	18.1	1049	6	US-10-223-087-319	Sequence 319, App
c	113	26.6	18.1	1049	7	US-10-223-083-319	Sequence 319, App
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c	115	26.6	18.1	1049	7	US-10-035-977-75	Sequence 75, Appli

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OM nucleic - nucleic search, using sw model

Run on: July 1, 2006, 04:39:12 ; Search time 152.627 Seconds
(without alignments)
1138.902 Million cell updates/sec

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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c 2	28.6	19.5	1189	7 US-11-266-748A-247034	Sequence 247034,
c 3	27.8	18.9	735	6 US-10-566-644-359	Sequence 359, App
4	27.6	18.8	1109	6 US-10-953-349-32969	Sequence 32969, A
5	26.8	18.2	4961	7 US-11-266-748A-32707	Sequence 32707, A
6	26.8	18.2	4964	7 US-11-266-748A-58994	Sequence 58994, A
7	26.8	18.2	97630	7 US-11-266-748A-29025	Sequence 29025, A
8	26.8	18.2	1071650	7 US-11-266-748A-22664	Sequence 22664, A
c 9	26.6	18.1	1000	7 US-11-266-748A-224413	Sequence 224413,
c 10	26.6	18.1	1000	7 US-11-266-748A-405342	Sequence 405342,
11	26.6	18.1	1000	7 US-11-266-748A-476388	Sequence 476388,
c 12	26.6	18.1	1015	7 US-11-266-748A-31476	Sequence 31476, A
c 13	26.6	18.1	1640	6 US-10-449-902-14082	Sequence 14082, A
c 14	26.2	17.8	1708	7 US-11-266-748A-36233	Sequence 36233, A
c 15	26	17.7	1242	7 US-11-266-748A-99285	Sequence 99285, A
16	26	17.7	1242	7 US-11-266-748A-152096	Sequence 152096,
17	26	17.7	1481	6 US-10-449-902-10729	Sequence 10729, A
c 18	26	17.7	2013	7 US-11-266-748A-32493	Sequence 32493, A
19	25.6	17.4	1408	6 US-10-449-902-18539	Sequence 18539, A
20	25.6	17.4	1437	7 US-11-266-748A-180422	Sequence 180422,
21	25.4	17.3	1000	7 US-11-266-748A-208379	Sequence 208379,
22	25.4	17.3	1000	7 US-11-266-748A-392666	Sequence 392666,
c 23	25.4	17.3	1000	7 US-11-266-748A-483384	Sequence 483384,
24	25.4	17.3	1003	7 US-11-266-748A-72875	Sequence 72875, A
c 25	25.4	17.3	1003	7 US-11-266-748A-125686	Sequence 125686,
c 26	25.4	17.3	1300	7 US-11-266-748A-415229	Sequence 415229,
c 27	25.4	17.3	1896	6 US-10-449-902-26217	Sequence 26217, A
c 28	25.4	17.3	1896	6 US-10-449-902-28382	Sequence 28382, A
29	25.4	17.3	1898	7 US-11-216-545-5274	Sequence 5274, Ap
c 30	25.2	17.1	1000	7 US-11-266-748A-293680	Sequence 293680,
31	25.2	17.1	1000	7 US-11-266-748A-345109	Sequence 345109,
c 32	25.2	17.1	1000	7 US-11-266-748A-405773	Sequence 405773,
33	25.2	17.1	1000	7 US-11-266-748A-476819	Sequence 476819,
c 34	25	17.0	396	7 US-11-266-748A-169854	Sequence 169854,
c 35	25	17.0	761	7 US-11-266-748A-367009	Sequence 367009,
36	25	17.0	761	7 US-11-266-748A-450388	Sequence 450388,
37	25	17.0	1031	7 US-11-266-748A-187145	Sequence 187145,
38	25	17.0	1156	6 US-10-449-902-21323	Sequence 21323, A
c 39	25	17.0	1230	7 US-11-266-748A-86048	Sequence 86048, A
40	25	17.0	1230	7 US-11-266-748A-138859	Sequence 138859,
41	25	17.0	1748	6 US-10-449-902-18103	Sequence 18103, A
42	25	17.0	2049	6 US-10-449-902-9609	Sequence 9609, Ap
c 43	25	17.0	2083	6 US-10-449-902-5382	Sequence 5382, Ap
44	25	17.0	2522	6 US-10-449-902-2969	Sequence 2969, Ap
45	25	17.0	2558	6 US-10-449-902-22605	Sequence 22605, A
46	25	17.0	3315	6 US-10-449-902-25062	Sequence 25062, A
c 47	24.8	16.9	847	7 US-11-266-748A-15048	Sequence 15048, A
c 48	24.8	16.9	847	7 US-11-266-748A-176197	Sequence 176197,
c 49	24.8	16.9	847	7 US-11-266-748A-362866	Sequence 362866,
c 50	24.8	16.9	847	7 US-11-266-748A-388001	Sequence 388001,
51	24.8	16.9	847	7 US-11-266-748A-446245	Sequence 446245,
c 52	24.8	16.9	848	7 US-11-266-748A-252684	Sequence 252684,
c 53	24.8	16.9	848	7 US-11-266-748A-275965	Sequence 275965,
54	24.8	16.9	848	7 US-11-266-748A-313201	Sequence 313201,
c 55	24.8	16.9	905	7 US-11-266-748A-74067	Sequence 74067, A
c 56	24.8	16.9	905	7 US-11-266-748A-108165	Sequence 108165,
57	24.8	16.9	905	7 US-11-266-748A-126878	Sequence 126878,
c 58	24.8	16.9	151830	6 US-10-519-335-37	Sequence 37, Appl
59	24.6	16.7	447	7 US-11-266-748A-354592	Sequence 354592,

60	24.6	16.7	447	7	US-11-266-748A-384944	Sequence 384944,
c 61	24.6	16.7	447	7	US-11-266-748A-437971	Sequence 437971,
c 62	24.6	16.7	473	7	US-11-266-748A-90451	Sequence 90451, A
63	24.6	16.7	473	7	US-11-266-748A-143262	Sequence 143262,
64	24.6	16.7	745	7	US-11-266-748A-211167	Sequence 211167,
c 65	24.6	16.7	745	7	US-11-266-748A-234893	Sequence 234893,
66	24.6	16.7	938	6	US-10-449-902-28314	Sequence 28314, A
c 67	24.6	16.7	1000	7	US-11-266-748A-288543	Sequence 288543,
68	24.6	16.7	1000	7	US-11-266-748A-339972	Sequence 339972,
c 69	24.6	16.7	1000	7	US-11-266-748A-399429	Sequence 399429,
70	24.6	16.7	1000	7	US-11-266-748A-470475	Sequence 470475,
71	24.6	16.7	1223	6	US-10-449-902-10809	Sequence 10809, A
c 72	24.6	16.7	1250	7	US-11-266-748A-175239	Sequence 175239,
c 73	24.6	16.7	1337	7	US-11-266-748A-255675	Sequence 255675,
c 74	24.6	16.7	1337	7	US-11-266-748A-277540	Sequence 277540,
75	24.6	16.7	1337	7	US-11-266-748A-316192	Sequence 316192,
c 76	24.6	16.7	1404	7	US-11-266-748A-15317	Sequence 15317, A
c 77	24.6	16.7	1404	7	US-11-266-748A-20967	Sequence 20967, A
c 78	24.6	16.7	1790	7	US-11-266-748A-74976	Sequence 74976, A
c 79	24.6	16.7	1790	7	US-11-266-748A-108664	Sequence 108664,
80	24.6	16.7	1790	7	US-11-266-748A-127787	Sequence 127787,
c 81	24.6	16.7	2010	7	US-11-266-748A-354590	Sequence 354590,
c 82	24.6	16.7	2010	7	US-11-266-748A-384942	Sequence 384942,
83	24.6	16.7	2010	7	US-11-266-748A-437969	Sequence 437969,
c 84	24.6	16.7	2156	7	US-11-266-748A-187932	Sequence 187932,
c 85	24.6	16.7	3350	7	US-11-266-748A-58152	Sequence 58152, A
c 86	24.6	16.7	4253	7	US-11-266-748A-57328	Sequence 57328, A
c 87	24.6	16.7	5726	7	US-11-266-748A-59367	Sequence 59367, A
88	24.6	16.7	59339	7	US-11-266-748A-23499	Sequence 23499, A
c 89	24.6	16.7	163319	7	US-11-266-748A-23968	Sequence 23968, A
c 90	24.4	16.6	317	7	US-11-266-748A-377210	Sequence 377210,
91	24.4	16.6	317	7	US-11-266-748A-460589	Sequence 460589,
c 92	24.4	16.6	343	7	US-11-266-748A-306061	Sequence 306061,
c 93	24.4	16.6	422	7	US-11-266-748A-425895	Sequence 425895,
94	24.4	16.6	499	6	US-10-488-619-2955	Sequence 2955, Ap
95	24.4	16.6	983	6	US-10-449-902-3932	Sequence 3932, Ap
c 96	24.4	16.6	1366	6	US-10-953-349-27435	Sequence 27435, A
97	24.4	16.6	1422	6	US-10-449-902-18774	Sequence 18774, A
c 98	24.2	16.5	394	7	US-11-266-748A-302848	Sequence 302848,
c 99	24.2	16.5	827	6	US-10-449-902-8980	Sequence 8980, Ap
100	24.2	16.5	839	7	US-11-266-748A-371962	Sequence 371962,
101	24.2	16.5	839	7	US-11-266-748A-389402	Sequence 389402,
c 102	24.2	16.5	839	7	US-11-266-748A-455341	Sequence 455341,
103	24.2	16.5	955	7	US-11-266-748A-171537	Sequence 171537,
c 104	24.2	16.5	955	7	US-11-266-748A-245364	Sequence 245364,
c 105	24.2	16.5	1721	6	US-10-953-349-1855	Sequence 1855, Ap
106	24.2	16.5	2030	6	US-10-449-902-4908	Sequence 4908, Ap
107	24.2	16.5	2257	6	US-10-449-902-26977	Sequence 26977, A
108	24.2	16.5	2336	6	US-10-449-902-20064	Sequence 20064, A
c 109	24	16.3	729	7	US-11-266-748A-361605	Sequence 361605,
c 110	24	16.3	729	7	US-11-266-748A-387695	Sequence 387695,
111	24	16.3	729	7	US-11-266-748A-444984	Sequence 444984,
c 112	24	16.3	736	7	US-11-216-545-8129	Sequence 8129, Ap
c 113	24	16.3	811	7	US-11-266-748A-80604	Sequence 80604, A
c 114	24	16.3	811	7	US-11-266-748A-110877	Sequence 110877,
115	24	16.3	811	7	US-11-266-748A-133415	Sequence 133415,
c 116	24	16.3	1338	7	US-11-217-529-2223	Sequence 2223, Ap
c 117	24	16.3	1820	6	US-10-449-902-25726	Sequence 25726, A
c 118	24	16.3	2602	6	US-10-449-902-28180	Sequence 28180, A
119	24	16.3	4339	6	US-10-449-902-24429	Sequence 24429, A
120	23.8	16.2	193	7	US-11-266-748A-427336	Sequence 427336,

SCORE Search Results Details for Application 10630536 and Search Result us-10-630-536- 8.rst.

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OM nucleic - nucleic search, using sw model

Run on: July 1, 2006, 04:17:07 ; Search time 5332.44 Seconds
(without alignments)
1541.534 Million cell updates/sec

Title: US-10-630-536-8

Perfect score: 147

Sequence: 1 atttgtcggaaagggtcgcatg.....ccgtcagaaagtcatcgacg 147

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : EST:
1: gb_est1:
2: gb_est3:
3: gb_est4:
4: gb_est5:
5: gb_est6:
6: gb_htc:
7: gb_est2:
8: gb_est7:
9: gb_est8:
10: gb_est9:
11: gb_gss1:
12: gb_gss2:
13: gb_gss3:
14: gb_gss4:

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Query					Description
		Score	Match	Length	DB	ID	
c	1	32.4	22.0	218	10	N83118	N83118 TgESTzy73g0
	2	32.2	21.9	671	8	CO236707	CO236707 WS0024.B2
c	3	31.4	21.4	614	3	BQ507186	BQ507186 EST614601
c	4	31.4	21.4	614	5	CK861660	CK861660 32764 In
c	5	31	21.1	643	5	CF642183	CF642183 D48_F07 F
c	6	31	21.1	1269	6	CNS0FROA	CR685230 Tetraodon
c	7	30.8	21.0	364	1	AV639843	AV639843 AV639843
	8	30.8	21.0	597	2	BI939652	BI939652 dad27f11.
c	9	30.6	20.8	278	8	CO827214	CO827214 LM_GB5_00
c	10	30.4	20.7	767	14	DU992819	DU992819 OG_ABa011
c	11	30.4	20.7	875	2	BM423055	BM423055 PLATE1_E1
c	12	30.2	20.5	474	5	CD888991	CD888991 G118.110L
c	13	30.2	20.5	709	12	CG362920	CG362920 OG2AY29TH
c	14	30.2	20.5	749	2	BJ722261	BJ722261 BJ722261
c	15	30.2	20.5	779	12	CC684152	CC684152 OGOBP18TH
c	16	30.2	20.5	793	12	CG346403	CG346403 OG0GC15TV
	17	30.2	20.5	823	10	DR829764	DR829764 ZM_BFb007
	18	30.2	20.5	836	12	CC335372	CC335372 OGTAH40TV
c	19	30.2	20.5	939	13	CZ384934	CZ384934 ZMMBF0160
c	20	30.2	20.5	941	12	CC383159	CC383159 PUHQC39TB
c	21	30.2	20.5	955	12	CG226597	CG226597 OG0GB14TV
	22	30.2	20.5	956	12	CC383161	CC383161 PUHQC39TD
c	23	30	20.4	1150	10	DW027829	DW027829 CFW241-H0
c	24	29.8	20.3	613	4	CA257585	CA257585 SCCCFL109
c	25	29.8	20.3	809	14	DX024030	DX024030 KBrB018J0
c	26	29.8	20.3	1038	10	DW656520	DW656520 CLJ395-N0
c	27	29.8	20.3	1272	4	CB598012	CB598012 AGENCOURT
c	28	29.6	20.1	420	2	BI727284	BI727284 1031091C0
c	29	29.6	20.1	510	7	BE129451	BE129451 894023C08
c	30	29.6	20.1	517	2	BM000798	BM000798 1031091C0
	31	29.6	20.1	526	8	CN914843	CN914843 030115ABN
	32	29.6	20.1	537	8	CN902820	CN902820 021015ABC
	33	29.6	20.1	577	8	CN914714	CN914714 030110ABN
	34	29.6	20.1	581	8	CN887254	CN887254 010512AAW
c	35	29.6	20.1	654	3	BQ812592	BQ812592 1030031B0
c	36	29.6	20.1	783	10	DT061731	DT061731 AGENCOURT
	37	29.4	20.0	471	8	CO329331	CO329331 EK292624.
c	38	29.4	20.0	516	8	CO344170	CO344170 EP18764.3
	39	29.4	20.0	608	8	CN897524	CN897524 010701AAZ
c	40	29.4	20.0	622	2	BJ071236	BJ071236 BJ071236
c	41	29.4	20.0	690	10	DT055649	DT055649 AGENCOURT
c	42	29.4	20.0	692	8	CN130245	CN130245 RHOH1_40_
c	43	29.4	20.0	695	10	DT062641	DT062641 AGENCOURT
	44	29.4	20.0	851	10	DR560924	DR560924 WS02620.C
c	45	29.4	20.0	857	3	BU901960	BU901960 AGENCOURT
c	46	29.4	20.0	902	4	CA972665	CA972665 AGENCOURT
c	47	29.4	20.0	987	14	CNS079PI	AL435580 T7 end of
	48	29.2	19.9	538	5	CK349793	CK349793 hggfha18A
	49	29.2	19.9	588	4	CB375197	CB375197 ru98g01.y
	50	29.2	19.9	612	11	BZ250355	BZ250355 CH230-448
	51	29.2	19.9	650	9	CX353284	CX353284 ssalrgb53
	52	29.2	19.9	748	14	DX103828	DX103828 MUGQ_CH25
	53	29.2	19.9	770	5	CK351523	CK351523 hggfha39D

c	54	29.2	19.9	779	5	CK187745	CK187745 EST777060
c	55	29.2	19.9	781	12	CG287393	CG287393 OG0BH92TH
c	56	29.2	19.9	817	5	CK699860	CK699860 ZF101-P00
c	57	29.2	19.9	832	12	BZ799294	BZ799294 PUFGN83TD
c	58	29.2	19.9	844	12	CG377903	CG377903 OGYAR73TV
c	59	29.2	19.9	847	12	CG276600	CG276600 OGZBG93TH
	60	29.2	19.9	849	12	CG287400	CG287400 OG0BH92TV
c	61	29	19.7	653	2	BI956991	BI956991 HVSMEn000
c	62	29	19.7	1017	11	BZ563071	BZ563071 pacs2-164
	63	28.8	19.6	323	1	AA084793	AA084793 zn13b01.r
c	64	28.8	19.6	388	2	BJ922159	BJ922159 BJ922159
c	65	28.8	19.6	423	10	N81852	N81852 TgESTzy48h0
	66	28.8	19.6	430	1	AM138865	AM138865 AM138865
	67	28.8	19.6	435	2	BJ909573	BJ909573 BJ909573
	68	28.8	19.6	519	1	AM139451	AM139451 AM139451
	69	28.8	19.6	567	13	CZ793062	CZ793062 OC_Ba016
c	70	28.8	19.6	573	4	CB389408	CB389408 OSTF116G7
	71	28.8	19.6	613	10	DV546594	DV546594 rbcma0_00
	72	28.8	19.6	690	8	CN476307	CN476307 SPVD11d08
c	73	28.8	19.6	691	9	DN096532	DN096532 JGI_CABE6
	74	28.8	19.6	705	9	DR093951	DR093951 STRR1_11
c	75	28.8	19.6	724	2	BJ538110	BJ538110 BJ538110
c	76	28.8	19.6	736	2	BJ534435	BJ534435 BJ534435
c	77	28.8	19.6	745	2	BJ541750	BJ541750 BJ541750
	78	28.8	19.6	749	3	BW447274	BW447274 BW447274
	79	28.8	19.6	749	9	DR093883	DR093883 STRR1_11
c	80	28.8	19.6	766	2	BJ723178	BJ723178 BJ723178
c	81	28.8	19.6	792	9	DR020365	DR020365 STRS1_36
	82	28.8	19.6	798	9	DR100271	DR100271 STRR1_63
c	83	28.8	19.6	808	9	DR101188	DR101188 STRR1_71
c	84	28.8	19.6	817	2	BG719203	BG719203 602690258
	85	28.8	19.6	818	9	CX806778	CX806778 JGI_CAAJ1
	86	28.8	19.6	830	9	DR100474	DR100474 STRR1_64
c	87	28.8	19.6	836	9	DR025068	DR025068 STRS1_69
	88	28.8	19.6	839	9	CX713116	CX713116 RTPQ1_7_C
	89	28.8	19.6	840	9	CX713197	CX713197 RTPQ1_7_C
	90	28.8	19.6	840	9	DR016857	DR016857 STRS1_12
	91	28.8	19.6	845	9	DR097239	DR097239 STRR1_33
c	92	28.8	19.6	858	9	DR020300	DR020300 STRS1_36
c	93	28.8	19.6	890	9	CX814195	CX814195 JGI_CAAJ2
c	94	28.8	19.6	944	2	BJ741548	BJ741548 BJ741548
	95	28.6	19.5	276	3	BP383858	BP383858 BP383858
c	96	28.6	19.5	379	3	BQ074085	BQ074085 fz31e09.y
	97	28.6	19.5	417	8	CO189699	CO189699 EK044927.
	98	28.6	19.5	545	10	DV228474	DV228474 EST-AR162
	99	28.6	19.5	574	14	DE050917	DE050917 Oryzias l
c	100	28.6	19.5	578	11	AQ600063	AQ600063 HS_5354_B
c	101	28.6	19.5	582	8	CV439602	CV439602 EST893515
c	102	28.6	19.5	610	9	DA531428	DA531428 DA531428
	103	28.6	19.5	752	10	DR645264	DR645264 EST103588
c	104	28.6	19.5	806	11	BH707579	BH707579 BOMNO31TF
	105	28.6	19.5	895	10	DR675509	DR675509 EST106562
	106	28.6	19.5	901	2	BG251828	BG251828 602364443
	107	28.6	19.5	919	10	DR645378	DR645378 EST103600
	108	28.6	19.5	942	10	DR660636	DR660636 EST105075
c	109	28.6	19.5	1097	9	DR135739	DR135739 49291272
	110	28.6	19.5	1156	10	DW037105	DW037105 CFW270-C0
	111	28.4	19.3	210	8	CX244595	CX244595 A59 cDNA-
c	112	28.4	19.3	346	4	BY021829	BY021829 BY021829
c	113	28.4	19.3	432	4	CB543200	CB543200 PVEPSE302
	114	28.4	19.3	459	3	BP175592	BP175592 BP175592